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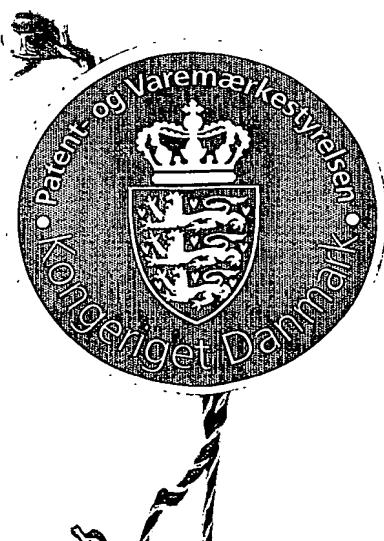
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Title: Surface-located Campylobacter jejuni polypeptides

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Patent- og Varemærkestyrelsen
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Susanne Morsing

PATENT- OG VAREMÆRKESTYRELSEN

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P814 DK00

1

Patent- og
Varemærkestyrelsen

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Modtaget

Surface-located *Campylobacter jejuni* polypeptides**Field of the invention**

The present invention relates to cell-surface-located polypeptides of *Campylobacter jejuni* and to fragments and variants thereof. Furthermore, the invention relates to polynucleotides encoding the polypeptides of the invention, and to vectors and recombinant viruses or recombinant cells expressing these. The invention also relates to use of the polypeptides and of antibodies directed against these in passive and active immunisation/vaccination and in diagnostic methods. Use of the polypeptides of the invention in methods for the identification of compounds with anti-*Campylobacter jejuni* activity is also described.

Background of the inventionOccurrence of *Campylobacter* infections

Campylobacter, a Gram-negative microaerophilic bacterium, was first identified as a human pathogen in 1973. It has since become the most common bacterial cause of diarrhoeal illness in the developed world, causing more disease than the more traditionally recognised food-borne pathogens, *Shigella* species (spp.) and *Salmonella* spp. combined. Of the different disease-causing *Campylobacter* strains, *C. jejuni* is the most important, being responsible for 99% of cases of campylobacteriosis. At a global level, surveillance has indicated a steady rise in the number of reported cases of campylobacteriosis since this organism was first recognised as a pathogen. Indeed, the World Health Organisation now recognises bacteria causing campylobacteriosis to be the most important agents of enteritis in the world. International public health officials estimate that *C. jejuni* alone causes 400 to 500 million cases of diarrhoea world-wide each year, and it is the number one food-borne pathogen in the U.S. Recent data for the year 2000 illustrate the significance of *Campylobacter* with respect to other more publicised causes of food borne illness. *Campylobacter* accounts for more cases, hospitalisations and deaths than *Salmonella* or *E. coli*-mediated food-borne illnesses. Amongst the data set, *Campylobacter* accounts for greater than 55% of cases and 33% of hospitalisations.

Symptoms of *Campylobacter* infections

Diarrhoea is the most consistent and prominent manifestation of campylobacteriosis. It is often bloody. Typical symptoms of *C. jejuni* infection also include fever, nausea,

P814 DK00

2

vomiting, abdominal pain, headache, and muscle pain. A majority of cases are mild and do not require hospitalisation and may be self-limited. However, *C. jejuni* infection can be severe and life-threatening. Death is more common when other diseases (e.g. cancer, liver disease, and immunodeficiency-related diseases) are present.

5 Children under the age of five and young adults aged 15-29 are the age groups most frequently affected. The incubation period (the time between exposure or onset of the first symptom) is typically two to five days, but onset may occur in as few as 2 days or as long as 10 days after ingestion. The illness usually lasts no more than one week; however, severe cases may persist for up to three weeks (CDC
10 Guidelines for confirmation of food-borne disease outbreaks. MMWR, 1996; 45:59).

Long-term consequences of Campylobacter

Campylobacter infection can sometimes have long-term consequences. Some patients may develop a disease, called Guillain-Barré syndrome, that affects the nerves of the body following campylobacteriosis. Although rare, it is the most common cause of acute generalised paralysis in the Western world. It begins several weeks after the diarrhoeal illness in a small minority of Campylobacter patients. It occurs when a person's immune system generates antibodies against components of Campylobacter and these antibodies attack components of the body's nerve cells because they are chemically similar to bacterial components.¹ Guillain-Barré syndrome begins in the feet and spreads up the body. Prickling sensations give way to weakness that may lead to paralysis. It lasts for weeks to months and often requires intensive care. Full recovery is common, however patients may be left with severe neurological damage. Approximately 15% of Guillain-Barré patients remain bedridden or wheelchair-bound after one year. It is estimated that approximately one in every 1000 (0.1%) reported campylobacteriosis cases leads to Guillain-Barré syndrome. As many as 40% of Guillain-Barré syndrome cases in the UK occur following campylobacteriosis.²

Miller Fisher Syndrome is another, related neurological syndrome that can follow campylobacteriosis and is also caused by immunologic mimicry.¹ In Miller Fisher syndrome, the nerves of the head are affected more than the nerves of the body.

Another chronic condition that may be associated with Campylobacter infection is an arthritis called Reiter's syndrome: This is a reactive arthritis that most commonly affects large weight-bearing joints such as the knees and the lower back.

P814 DK00

3

It is a complication that is strongly associated with a particular genetic make-up; persons who have the human lymphocyte antigen B27 (HLA-B27) are most susceptible.

In addition, *Campylobacter* may also cause appendicitis or infect the abdominal cavity (peritonitis), the heart (carditis), the central nervous system (meningitis), the gallbladder (cholecystitis) the urinary tract, and the blood stream.

References:

1. Ang CW et al. (2001) Infect Immun.69(4):2462-2469.
2. Rees et al. (1995) N Engl J Med 333:1374-1379.

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Treatment of campylobacteriosis

Patients with campylobacteriosis should drink plenty of fluids as long as the diarrhoea lasts in order to maintain hydration. Antidiarrhoeal medications such as loperamide may allay some symptoms. *Campylobacter* is usually a self-limited illness, but when it is identified, specific treatment with antibiotics is indicated, as treatment may shorten the course of the illness. In more severe cases of gastroenteritis, antibiotics are usually begun before culture results are known. Macrolide antibiotics (erythromycin, clarithromycin, or azithromycin) are the most effective agents for *C. jejuni*. Fluoroquinolone antibiotics (ciprofloxacin, levofloxacin, gatifloxacin, or moxifloxacin) can also be used.

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However, resistance of *Campylobacter* to antimicrobial agents has been reported in many countries and is on the rise (Pedington and Kaneene (2003) J. Vet. Med. Sci. 65(2):161-170). Quinolone-resistance is on the rise in Europe, Asia and the US. The increase of resistance is at least partially related to the use of antibiotics in poultry feed (Smith et al. (1999) N Engl J Med 340:1525-1532).

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Novel strategies for the treatment, prevention and diagnosis of Campylobacter

P814 DK00

4

crobiology, pp. 303-319). In addition, there is a need for novel rapid and reliable methods for diagnosis of *Campylobacter* infections.

These objectives can be accomplished through the identification and use of suitable *Campylobacter jejuni* polypeptides that can function as targets, i.e. targets for the immune system and/or for antibodies, targets for cytotoxic inhibitors, or targets for indicator moieties in diagnosis.

Summary of the invention

The present application relates to surface-located polypeptides of *Campylobacter jejuni*. In the context of this application, a 'surface-located' polypeptide is defined as a polypeptide which is at least partially (i.e. part of the polypeptide chain and/or part of the population of polypeptide molecules) localised outside the outer membrane of a *Campylobacter jejuni* cell. Thus, a surface-located polypeptide is a polypeptide which is fully or partially exposed to the space outside the outer-membrane. Surface-located polypeptides furthermore include all polypeptides or polypeptide fragments that can be identified in fractions obtained by low-pH surface-protein extraction as described herein.

Surface-located polypeptides are attractive targets for antibacterial therapy and/or diagnosis of bacterial infection, since the exposure of such polypeptides to the extracellular space means that compounds that interact with these polypeptides (e.g. compounds used to prevent, treat or diagnose bacterial infections) often do not need to enter or pass the outer membrane to be effective.

The determination of cell-surface localisation of a *Campylobacter jejuni* polypeptide can at present only be done experimentally and not by bioinformatics, as no common sorting signals or motifs are known for this localisation. It is possible to predict with some degree of certainty whether or not polypeptides enter the periplasm, but no general motif has been identified for surface-localisation of polypeptides, and therefore it is not possible to predict from the sequence alone whether any given periplasmic (or non-periplasmic) polypeptide will be transported to the surface. The number of confirmed surface polypeptides is relatively low in *Campylobacter jejuni* and includes mostly flagella structural proteins and a small number of non-flagella related surface proteins, such as PEB1-4.

The Inventors have identified 51 different polypeptides in cell-surface fractions of *Campylobacter jejuni*. The method that was employed identifies polypeptides that are expressed at a relatively high level. The combination of being surface-

P814 DK00

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exposed and being present in relatively high amounts makes these polypeptide highly suitable as targets for antibodies and thus for use in passive or active immunisation/vaccination. Fifteen of the 51 surface-located polypeptides that were identified (SEQ ID NO:37-51) have previously been described amongst more than 5 36,000 other loci as hits in homology searches using essential genes from other bacteria, see WO 02/077183. While WO 02/077183 is mostly directed towards inhibition of gene expression using antisense constructs, WO 02/077183 also describes the possibility of generating antibodies specific for any of the more than 36,000 polypeptides and the possibility of generating an immune response using 10 any of the more than 36,000 polypeptides. However, WO 02/077183 does not describe an identification of the subcellular localisation of the identified polypeptides nor a determination of their expression levels. Thus, since most of the more than 36,000 polypeptides will not be surface-exposed and/or not expressed at sufficient 15 levels, the large majority of the polypeptides identified in WO 02/077183 will not be suitable for generating a protective immune response in a host organism, because antibodies directed against them will not bind to an intact bacterial cell and/or because too few binding sites will be present per cell. Thus, the teaching of WO 02/077183 does not enable the skilled person to identify the minority of polypeptides amongst the more 36,000 that can be used to generate a protective immune 20 response.

The combination of being surface-exposed and being present in relatively high amounts also makes the 51 polypeptides identified by the Inventors highly suitable as targets for diagnosis of campylobacteriosis, allowing detection of intact cells with high sensitivity. In addition, the surface-localisation of the 51 polypeptides makes them suitable as targets for inhibitors. Such inhibitors may be bactericidal or bacteriostatic or prevent interaction of *Campylobacter jejuni* with the host organism (virulence).

Definitions

30 - Vaccine - is used to indicate a composition capable of inducing a protective immune response against a microorganism in a human being or animal.

 - Protective immune response - is used to indicate an immune response (humoral/antibody and/or cellular) inducing memory in an organism, resulting in the infectious agent, herein *Campylobacter jejuni*, being met by a secondary rather 35 than a primary response, thus reducing its impact on the host organism.

- Polypeptide – unless specified otherwise, the term 'polypeptide' when used herein can also refer to a variant or fragment of a polypeptide. Preferred polypeptides are antigenic polypeptides.
- 5 - Fragment – is used to indicate a non-full length part of a polypeptide. Thus, a fragment is itself also a polypeptide.
- Variant – a 'variant' of a given reference polypeptide refers to a polypeptide that displays a certain degree of sequence identity to said reference polypeptide but is not identical to said reference polypeptide.
- 10 - Antigen / antigenic / antigenicity / immunogen / immunogenic / immunogenicity – all refer to the capability of inducing an immune response.
- Immunogenic carrier – refers to a compound which directly or indirectly assists or strengthens an immune response.
- 15 - Expression vector - refers to a, preferably recombinant, plasmid or phage or virus to be used in production of a polypeptide from a polynucleotide sequence. An expression vector comprises an expression construct, comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and which is operably linked to the elements of (1); and (3) appropriate transcription initiation and termination sequences.
- 20 - Binding partner - of a polypeptide refers to a molecule that can bind to said polypeptide. Such binding can be indirect, through another molecule, but is preferably direct. A binding partner can be any type of molecule, such as e.g. small hydrophobic molecules or e.g. a cellular or extracellular macromolecule, such as a protein, a carbohydrate or a nucleic acid. Preferred types of binding partners include antibodies, ligands or inhibitors.
- Plurality - the term 'plurality' indicates more than one, preferably more than 10.
- Indicator moiety - the term 'indicator moiety' covers a molecule or a complex of molecules that is capable of specifically binding a given polypeptide and/or cell, and is capable of generating a detectable signal. Preferably, the indicator moiety is an antibody or includes an antibody molecule. Thus, a preferred indicator moiety is an antibody coupled to or in complex with a detectable substance.
- 30 - Host-derived molecule or host molecule - refers to a molecule which is normally found in a host organism that can be infected with *C. jejuni*. A host-derived molecule is preferably a host polypeptide, preferably a human polypeptide.
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P814 DK00

7

- Antibody - the term 'antibodies' when used herein is intended to cover antibodies as well as functional equivalents thereof. Thus, this includes polyclonal antibodies, monoclonal antibodies (mAbs), humanised, human or chimeric antibodies, single-chain antibodies, and also binding fragments of antibodies, such as Fab fragments, $F(ab')_2$ fragments, fragments produced by a Fab expression library, anti-idiotypic antibodies, hybrids comprising antibody fragments, and epitope-binding fragments of any of the these. The term also includes multivalent, multispecific, such as bispecific antibodies and mixtures of monoclonal antibodies.
- 5 - Dissociation constant, K_d , is a measure to describe the strength of binding (or affinity or avidity) between macromolecules, for example an antibody and its antigen. The smaller K_d the stronger binding.
- 10 - Isolated - used in connection with polypeptides and polynucleotides disclosed herein 'isolated' refers to these having been identified and separated and/or recovered from a component of their natural, typically cellular, environment. Contaminant components of the natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. Polypeptides and polynucleotides of the invention are preferably isolated, and vaccines and other compositions of the invention preferably comprise isolated polypeptides and/or isolated polynucleotides.
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Detailed description

Figures

25 Figure 1 and 2 show Western blot analyses using purified recombinant protein and dilutions of serum samples of immunised animals.

Vaccines and methods of vaccination of the invention

30 The goal of vaccination or active immunisation is to provide protective immunity by inducing a memory response to an infectious microorganism using an antigenic or immunogenic composition. Thus, a vaccine is a composition capable of inducing a protective immune response against a microorganism in a human being or animal. Such an immune response can be a cellular response and/or a humoral response, e.g. a specific T cell response or an antibody response.

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P814 DK00

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In a first main aspect, the present invention relates to a (recombinant) vaccine comprising a pharmaceutically-acceptable carrier and any one or more of the following:

- a polypeptide comprising a sequence having at least 95% sequence identity to any of the sequences selected from the group of surface-located *Campylobacter jejuni* polypeptides of SEQ ID NO:1-51, such as any of the sequences of SEQ ID NO:1-36 or any of the sequences of SEQ ID NO:37-51; or comprising an antigenic fragment of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
or
- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector.

15 In other words, the phrase:

'a polypeptide comprising a sequence having at least 95% sequence identity to any of the sequences selected from the group of surface-located *Campylobacter jejuni* polypeptides of SEQ ID NO:1-51, such as any of the sequences of SEQ ID NO:1-36 or any of the sequences of SEQ ID NO:37-51'

20 is directed to:

'a polypeptide comprising any of the sequences selected from the group of surface-located *Campylobacter jejuni* polypeptides of SEQ ID NO:1-51, such as any of the sequences of SEQ ID NO:1-36 or any of the sequences of SEQ ID NO:37-51 or a polypeptide comprising a variant of any of said sequences, wherein the variant has at least 95% sequence identity to said sequence.'

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30 The vaccine may only comprise one polypeptide selected from the group of SEQ ID NO:1-51 or a fragment or variant thereof. However, in other embodiments, the vaccine comprises more than one polypeptide of the group of SEQ ID NO:1-51 and/or more than one fragment of a polypeptide selected from the group of SEQ ID NO:1-51. Thus, the vaccine according to the invention may comprise more than one, such as 2, for example 3, such as 4, for example 5, such as 6, for example 7, such as 8, for example 9, such as 10, such as a number of polypeptides and/or fragments in the range of from 5 to 10, or more than 10, such as for example in the range of from

10 to 20, different polypeptides selected from the group of SEQ ID NO:1-51 or fragments thereof.

Similarly, the vaccine may only comprise one polynucleotide, one expression vector or one recombinant virus or recombinant cell of the invention. However, 5 In other embodiments, the vaccine comprises more than one polynucleotide, one expression vector or one recombinant virus or recombinant cell of the invention. Thus, the vaccine according to the invention may comprise more than one, such as 2, for example 3, such as 4, for example 5, such as 6, for example 7, such as 8, for example 9, such as 10, or more than 10, such as for example in the range of from 10 to 20, different polynucleotides, expression vectors or recombinant viruses or recombinant cells of the invention as described herein.

Furthermore, in some embodiments, a recombinant cell of the invention may express more than one polypeptide of the group of SEQ ID NO:1-51 and/or more than one fragment of a polypeptide selected from the group of SEQ ID NO:1-51. Thus, the vaccine according to the invention may comprise a recombinant cell comprising more than one, such as 2, for example 3, such as 4, for example 5, such as 6, for example 7, such as 8, for example 9, such as 10, such as a number of polypeptides and/or fragments in the range of from 5 to 10, or more than 10, such as for example in the range of from 10 to 20, different polypeptides selected from the 20 group of SEQ ID NO:1-51 or fragments thereof.

Vaccines comprising full-length polypeptides and/or fragments and/or variants

In preferred embodiments, the invention relates to a vaccine for prevention of infection with and/or development of disease from *Campylobacter jejuni* comprising any 25 of the polypeptides of SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51, or a fragment or variant thereof. Preferred fragments and variants are those described in the sections herein that relate to fragments and variants.

Accordingly, in these embodiments, the antigenicity or immunogenicity is provided by direct administration of a polypeptide normally located on the surface of 30 a *Campylobacter jejuni* cell. In one particular embodiment, the polypeptides are selected so that a vaccine comprises multiple polypeptides capable of associating with different MHC molecules, such as different MHC class I molecules. Preferably, a vaccine comprises polypeptides and/or fragments capable of associating with the most frequently occurring MHC class I molecules. In one particular embodiment of 35 the invention, the vaccine comprises one or more polypeptides and/or fragments

P814 DK00

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capable of associating to an MHC class I molecule and one or more polypeptides and/or fragments capable of associating with an MHC class II molecule. Hence, a vaccine is in some embodiments capable of raising a specific cytotoxic T-cells response and/or a specific helper T-cell response. Association to MHC molecules can 5 e.g. be determined as described by Andersen et al. (1999) *Tissue Antigens* 54:185; or by Tan et al. (1997) *J. Immunol. Methods* 209:25.

Adjuvants and immunogenic carriers

10 Preferably, vaccines of the present invention comprise a pharmaceutically-acceptable carrier as described herein in the section 'Compositions of the invention'.

The vaccine can further comprise an adjuvant. Adjuvants are substances whose admixture into the vaccine composition increases or otherwise modifies the immune response to a polypeptide. Adjuvants could for example be any of: AlK(SO₄)₂, AlNa(SO₄)₂, AlNH₄(SO₄), silica, alum, Al(OH)₃, Ca₃(PO₄)₂, kaolin, carbon, aluminium hydroxide, aluminium phosphate, muramyl dipeptides, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-DMP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (CGP 11687, also referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, also referred to as MTP-PE), RIBI (MPL+TDM+CWS) in 20 a 2% squalene/Tween-80.RTM. emulsion, lipopolysaccharides and derivatives, including lipid A, Freund's Complete Adjuvant (FCA), Freund's Incomplete Adjuvants, Merck Adjuvant 65, polynucleotides (for example, poly IC and poly AU acids), wax D from Mycobacterium, tuberculosis, substances found in *Corynebacterium parvum*, *Bordetella pertussis*, and members of the genus *Brucella*, liposomes or other lipid 25 emulsions, Titermax, ISCOMS, Quil A, ALUN (see US 58767 and 5,554,372), Lipid A derivatives, cholera toxin derivatives, HSP derivatives, LPS derivatives, synthetic peptide matrixes or GMDP, Interleukin 1, Interleukin 2, Montanide ISA-51 and QS-21. Preferred adjuvants to be used with the invention include Montanide ISA-51 and 30 QS-21. Montanide ISA-51 (Seppic, Inc.) is a mineral oil-based adjuvant analogous to incomplete Freund's adjuvant, which must be administered as an emulsion. QS-21 (Antigenics; Aquila Biopharmaceuticals, Framingham, MA) is a highly purified, water-soluble saponin that handles as an aqueous solution.

Desirable functionalities of adjuvants capable of being used in accordance with the present invention are listed in the below table.

Table 1 Modes of adjuvant action

Action	Adjuvant type	Benefit
1. Immunomodulation	Generally small molecules or proteins which modify the cytokine network	Upregulation of immune response. Selection of Tfh or Th2
2. Presentation	Generally amphiphatic molecules or complexes which interact with immunogen in its native conformation	Increased neutralizing antibody responses. Greater duration of response
3. CTL induction	<ul style="list-style-type: none"> • Particles which can bind or encode immunogen and which can fuse with or disrupt cell membranes • w/o emulsions for direct attachment of peptide to cell surface MHC-I 	Cytosolic processing of protein yielding correct class I restricted peptides
4. Targeting	<ul style="list-style-type: none"> • Particulate adjuvants which bind immunogen. Adjuvants which saturate Kupffer cells • Carbohydrate adjuvants which target lectin receptors on macrophages and DCs 	Simple process if promiscuous peptide(s) known Efficient use of adjuvant and immunogen
5. Depot generation	<ul style="list-style-type: none"> • w/o emulsion for short term • Microspheres or nanoparticles for long term 	As above. May also determine type of response if targeting selective Efficiency Potential for single dose vaccine

Source: John C. Cox and Alan R. Coulter Vaccine 1997 Feb;15(3):248-56

A vaccine composition according to the present invention may comprise more than one different adjuvant. It is also contemplated that the *Campylobacter* polypeptide of the invention, or one or more fragments thereof, and the adjuvant can be administered separately in any appropriate sequence.

Frequently, the adjuvant of choice is Freund's complete or incomplete adjuvant, or killed *B. pertussis* organisms, used e.g. in combination with alum precipitated antigen. A general discussion of adjuvants is provided in Goding, Monoclonal Antibodies: Principles & Practice (2nd edition; 1986) at pages 61-63. Goding notes, however, that when the antigen of interest is of low molecular weight, or is poorly immunogenic, coupling to an immunogenic carrier is recommended (see below). Various saponin extracts and cytokines have also been suggested to be useful as adjuvants in immunogenic compositions. Recently, it has been proposed to use granulocyte-macrophage colony stimulating factor (GM-CSF), a well known cytokine, as an adjuvant (WO 97/28816).

In addition, a vaccine of the invention can comprise an immunogenic carrier such as a scaffold structure, for example a protein or a polysaccharide, to which the *Campylobacter* polypeptide or the fragment thereof is capable of being associated. A *Campylobacter* polypeptide, or the fragment thereof, present in the vaccine composition can be associated with an immunogenic carrier such as e.g. a protein. The association of the polypeptide to a carrier protein may be covalent or non-covalent. An immunogenic carrier protein may be present independently of an adjuvant. The function of a carrier protein can for example be to increase the molecular weight of in particular fragments in order to increase their activity or immunogenicity, to confer stability, to increase the biological activity, or to increase serum half-life. Furthermore, an immunogenic carrier protein may aid presenting the

P814 DK00

12

Campylobacter polypeptide or the fragments thereof to T-cells. A carrier protein could be, but is not limited to, keyhole limpet hemocyanin, serum proteins such as transferrin, bovine serum albumin, human serum albumin, thyroglobulin or ovalbumin, immunoglobulins, or hormones, such as insulin. Tetanus toxoid and/or diphtheria toxoid are also suitable carriers in one embodiment of the invention. Alternatively or additionally, dextrans, for example sepharose may be added. In yet another embodiment, an antigen-presenting cell such as e.g. a dendritic cell capable of presenting the polypeptide or a fragment thereof to a T-cell may be added to obtain the same effect as a carrier protein.

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Methods for the preparation of vaccines have e.g. been described in US 5,470,958 and references therein. An effective amount of the polypeptide component of a vaccine of the invention, if injected, will typically be in the range of from about 0.1 to about 1000 µg, such as e.g. from about 1 to about 900 µg, for example from about 5 to about 500 µg, for a human subject, and generally in the range of from about 0.01 to 10.0 µg/Kg body weight of a subject animal. The above-indicated ranges are merely indicative and should not be interpreted as limiting the present invention.

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An effective amount of an antigenic polypeptide of the invention may be an amount capable of eliciting a detectable humoral immune response in the absence of an immunomodulator. For many immunogens, this is in the range of about 5-100 µg for a human subject. The appropriate amount of immunogen to be used is dependent on the immunological response it is desired to elicit. Furthermore, the exact effective amount necessary will vary from subject to subject, depending on the species, age and general condition of the subject, the severity of the condition being treated, the mode of administration, etc. It is therefore not always possible to specify an exact effective amount. However, the appropriate effective amount may be determined by one of ordinary skill in the art using only routine experimentation or prior knowledge in the art.

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30 DNA vaccines and vaccines comprising recombinant viruses or recombinant cells
DNA or RNA vaccines pertain to the introduction of e.g. an antigenic polypeptide determinant into a patient by overexpressing in the cells of the patient a polynucleotide construct which includes expression control sequences operably linked to a

P814 DK00

13

sequence encoding the polypeptide of interest, herein a polypeptide of any of SEQ ID NO:1-51 or a variant or fragment thereof. As such fragments may not contain a methionine start codon, such a codon is optionally included as part of the expression control sequences. The polynucleotide construct may be a non-replicating and linear polynucleotide, a circular expression vector, or an autonomously replicating plasmid or viral expression vector. The construct may become integrated into the host genome. Any expression vector that can transfect a mammalian cell may be used in the methods of immunising an individual according to the present invention. Methods for constructing expression vectors are well known in the art (see, e.g., Molecular Cloning: A Laboratory Manual, Sambrook et al., eds., Cold Spring Harbor Laboratory, 2nd Edition, Cold Spring Harbor, N.Y., 1989). Preferred are vaccines comprising a plurality of genes expressing multiple polypeptides selected from SEQ ID NO:1-51 and/or multiple fragments of the invention, thereby permitting simultaneous vaccination against a variety of preselected targets.

Vaccines can also be prepared by incorporating a polynucleotide encoding a specific antigenic polypeptide of interest into a living but harmless vector, such as a virus or a cell, such as an attenuated or reduced-virulence *E. coli* or *Salmonella* cell. The harmless recombinant virus or recombinant cell is injected into the intended recipient. Such a recombinant cell may be dead or alive. If alive, the recombinant organism may replicate in the host while producing and presenting the antigenic polypeptide to the host's immune system. It is contemplated that this type of vaccine will be more effective than the non-replicative type of vaccine. For such a vaccine to be successful, the vector organism must be viable, and either be naturally non-virulent or have an attenuated or reduced-virulence phenotype.

Strategies for vaccination using attenuated bacteria and suitable bacterial strains for use therein have been described in e.g. Makino et al. (2001) *Microb. Pathog.* 31:1-8; Gentschev et al. (2002) *Int. J. Med. Microbiol.* 291:577-582; Turner et al. (2001) *Infect. Immun.* 69:4969-4979; WO99/49026; and WO03/022307.

Further examples of vectors that can be applied are vectors comprising e.g., retroviruses, as disclosed in WO 90/07936, WO 91/02805, WO 93/25234, WO 93/25698, and WO 94/03622, adenovirus, as disclosed by Berkner, *Biotechniques* 6:616-627, 1988; Li et al., *Hum. Gene Ther.* 4:403-409, 1993; Vincent et al., *Nat. Genet.* 5:130-134, 1993; and Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994), pox virus, as disclosed by U.S. 4,769,330; U.S. Pat. No. 5,017,487; and WO 89/01973, naked DNA as disclosed WO 90/11092, a polynucleotide molecule com-

P814 DK00

14

plexed to a polycationic molecule as disclosed in WO 93/03709, and polynucleotides associated with liposomes as disclosed by Wang et al., Proc. Natl. Acad. Sci. USA 84:7851; 1987. In certain embodiments, the DNA may be linked to killed or inactivated adenovirus as disclosed by Curiel et al., Hum. Gene Ther. 3:147-154, 5 1992; Cotton et al., Proc. Natl. Acad. Sci. USA 89:6094, 1992. Other suitable compositions include DNA-ligands as disclosed by Wu et al., J. Biol. Chem. 264:16985-16987, 1989), and lipid-DNA combinations as disclosed by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417, 1989). In addition, the efficiency of naked DNA uptake into cells may be increased by coating the DNA onto biodegradable latex 10 beads.

Vaccine vectors preferably comprise a suitable promoter which is operably linked to the polynucleotide sequence encoding the immunogenic polypeptide. Any promoter that can direct a high level of transcription initiation in the target cells may be used in the invention. Non-tissue specific promoters, such as the cytomegalovirus (DeBernardi et al., Proc Natl Acad Sci USA 88:9257-9261 [1991], and references therein), mouse metallothioneine I (Hammer et al., J Mol Appl Gen 1:273-288 [1982]), HSV thymidine kinase (McKnight, Cell 31:355-365 [1982]), and SV40 early (Benoist et al., Nature 290:304-310 [1981]) promoters may thus also be used.

20 Methods of vaccination

In a further main aspect, the present invention relates to the use of any one or more of

- a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51; or comprises a 25 fragment or variant of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector,

30 or

- a composition as defined herein,

for the preparation of a medicament for the immunisation of an animal or human being against *Campylobacter jejuni* infections.

Similarly, the invention relates to a method for the immunisation of an animal or human being against a *Campylobacter jejuni* infections comprising the step of administering any one or more of

- a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51; or comprises a fragment or variant of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector,

or

- a composition as defined herein.

The animal may be any bird or mammal, e.g. a chicken, duck, turkey, cow or pig. Particular target populations of human beings may be individuals from at-risk populations, such as the population of children up to 4 years old, the population of persons in industrialised nations or the population of naive or semi-immune travellers to the developing world.

Modes of administration of the composition according to the invention include, but are not limited to systemic administration, such as intravenous or subcutaneous administration, intradermal administration, intramuscular administration, intranasal administration, oral administration, and generally any form of mucosal administration.

The immunogenic effect according to the present invention can e.g. be measured by assay of antibodies in serum samples e.g. by a RIA. Furthermore, the effect can be determined *in vivo*, by measuring e.g. an increased T cell responsiveness to T cell dependent antigenic polypeptides, wherein said increased responsiveness is characteristic of an enhancement of a normal immune response to such antigenic polypeptides. An immunostimulating effect may also be measured as an enhanced T cell production of, in particular, IL-2, IL-3, IFN-γ and/or GM-CSF. Polypeptides or fragments thereof having a potential for eliciting an enhanced immune response may thus be readily identified by screening for enhanced IL-2, IL-3, IFN-γ or GM-CSF production by T cells, as described e.g. in US 07/779,499, incorporated herein by reference. Young et al. (2000) In: *Campylobacter*, 2nd ed. Ed. by Nachamkin and

P814 DK00

16

Blaser, American Society for Microbiology, pp. 287-301 also describe a series of suitable animal models which can be of use in the evaluation of the efficacy of therapeutic and preventive strategies and compositions. A number of aspects related to vaccination against *Campylobacter*, including potential target populations, 5 animal models and vaccination strategies have been described by Scott and Tribble (2000) In: *Campylobacter*, 2nd ed. Ed. by Nachamkin and Blaser, American Society for Microbiology, pp. 303-319).

The herein described polynucleotides and expression vectors can be introduced into target cells *in vivo* or *in vitro* by any standard method: e.g., as naked 10 DNA (Donnelly et al., *Annu Rev Immunol* 15:617-648 [1997]), incorporated into IS-COMS, liposomes, or erythrocyte ghosts, or by biolistic transfer, calcium precipitation, or electroporation. Alternatively, one can employ a viral-based vector as a means for introducing the polynucleotide encoding the polypeptide of interest into the cells of the animal or human being. Preferred viral vectors include those derived 15 from replication-defective hepatitis viruses (e.g., HBV and HCV), retroviruses (see, e.g., WO89/07136; and Rosenberg et al., *N Eng J Med* 323 (9):570-578 [1990]), adenovirus (see, e.g., Morsey et al., *J Cell Biochem, Supp.* 17E [1993]), adeno-associated virus (Kotin et al., *Proc Natl Acad Sci USA* 87:2211-2215 [1990]), replication defective herpes simplex viruses (HSV; Lu et al., Abstract, page 66, Abstracts 20 of the Meeting on Gene Therapy, Sep. 22-26, 1992, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.), canary pox virus, and any modified versions of these vectors. Cells transfected *in vitro* can be cultured and cloned, if desired, prior to introduction into the patient.

In addition to direct *in vivo* procedures, *ex vivo* procedures may be used in 25 which cells are removed from an animal, modified, and placed into the same or another animal. It will be evident that one can utilise any of the compositions noted above for introduction of an antigenic polypeptides or polynucleotides encoding such according to the invention into tissue cells in an *ex vivo* context. Protocols for viral, physical and chemical methods of uptake are well known in the art. Thus, as an alternative 30 to administration of a polypeptide of the invention or a vector capable of expressing such a polypeptide directly to the patient, one can remove helper T cells from the patient; stimulate those T cells *ex vivo* using the same antigenic polypeptide or vector; and introduce the stimulated helper T cells into the same patient.

P814 DK00

17

Antibodies and methods for raising antibodies of the Invention

In a further main aspect, the invention relates to antibodies capable of specifically (recognising and) binding any of the polypeptides of SEQ ID NO:1-36 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:1 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:2 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:3 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:4 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:5 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:6 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:7 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:8 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:9 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:10 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:11 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:12 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:13 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:14 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:15 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:16 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:17 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:18 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:19 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:20 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:21 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:22 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:23 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:24 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:25 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:26 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:27 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:28 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:29 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:30 and/or a fragment and/or a variant thereof,

P814 DK00

18

a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:31 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:32 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:33 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:34 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:35 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:36 and/or a fragment and/or a variant thereof.

In preferred embodiments, the antibodies of the invention are capable of specifically binding an intact *Campylobacter jejuni* cell, i.e. capable of binding a living or a dead *Campylobacter* cell which has maintained its structural integrity, preferably a cell that has maintained the integrity of the outer membrane (i.e. wherein the outer membrane is not permeabilised). Binding of antibodies to intact cells can e.g. be determined by flow cytometry as described in Rioux et al.(2001) Infect. Immun. 69:5162-5165 or as described in Singh et al. (2003) Infect. Immun. 71:3937-3946.

In another main aspect, the invention relates to an antibody capable of specifically (recognising and) binding an intact *Campylobacter jejuni* cell and capable of specifically binding any of the polypeptides of SEQ ID NO:37-51 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:37 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:38 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:39 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:40 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:41 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:42 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:43 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:44 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:45 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:46 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:47 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:48 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:49 and/or a fragment and/or a variant thereof, for example the polypeptide of SEQ ID NO:50 and/or a fragment and/or a variant thereof, such as the polypeptide of SEQ ID NO:51 and/or a fragment and/or a variant thereof.

P814 DK00

19

Preferred antibodies are ones that specifically bind with a dissociation constant or K_d less than $5 \times 10^{-6} M$, such as less than $10^{-6} M$, e.g. less than $5 \times 10^{-7} M$, such as less than $10^{-7} M$, e.g. less than $5 \times 10^{-8} M$, such as less than $10^{-8} M$, e.g. less than $5 \times 10^{-9} M$, such as less than $10^{-9} M$, e.g. less than $5 \times 10^{-10} M$, such as less than $10^{-10} M$, e.g. less than $5 \times 10^{-11} M$, such as less than $10^{-11} M$, e.g. less than $5 \times 10^{-12} M$, such as less than $10^{-12} M$, e.g. less than $5 \times 10^{-13} M$, such as less than $10^{-13} M$, e.g. less than $5 \times 10^{-14} M$, such as less than $10^{-14} M$, e.g. less than $5 \times 10^{-15} M$, or less than $10^{-15} M$. Binding constants can be determined using methods well-known in the art, such as ELISA (e.g. as described in Orosz and Ovadi (2002) J. Immunol. Methods 270:155-162) or surface plasmon resonance analysis.

Antibodies can be used for passive immunisation of mammals, preferably human beings, more preferably immunocompromised patients. A treatment with antibodies can be done to cure or to prevent *Campylobacter jejuni* infections.

Antibodies of the invention may be mechanistically divided into the following preferred groups:

1. Function-inhibiting antibodies that work as an antibacterial (affect the viability of the bacterium). Such antibodies should be effective regardless of the immune status of the patient. Preferably, such antibodies are capable of reducing *Campylobacter jejuni* growth in vitro to less than 50%, such as less than 25%, for example less than 10%, such as less than 5% of a control without antibody added.
2. Opsonising antibodies that are designed to enhance phagocytic killing. Effectiveness of such antibodies may depend on the immune status of the patient, but it is very well possible that they will enhance phagocytic killing even in compromised patients.
3. Antibodies conjugated to a therapeutic moiety such as a toxin or bactericidal agent, e.g. ricin or radiisotopes. Techniques for conjugating a therapeutic moiety to antibodies are well known, see, e.g. Thorpe et al.(1982) Immunol. Rev. 62, 119-158. These antibodies should also be effective regardless of the immune status of the patient.

An antibody with or without a therapeutic moiety conjugated to it can be used as a therapeutic that is administered alone or in combination with chemotherapeutics or other therapeutic agents.

P814 DK00

20

In a further main aspect, the invention relates to a method for raising specific antibodies to a polypeptide of any of SEQ ID NO:1-36 in an (non-human) animal comprising the steps of

a. providing

- 5 - a polypeptide comprising any of the sequences of SEQ ID NO:1-36, or comprising a fragment or variant thereof,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
 or
- 10 - a recombinant virus or recombinant cell of the invention as defined herein,

b. introducing a composition comprising said polypeptide, polynucleotide, vector or recombinant virus or recombinant cell into said animal,

c. raising antibodies in said animal, and

d. isolating and optionally purifying the antibodies.

15

A method for raising specific antibodies to a polypeptide of any of SEQ ID NO:37-51 in an (non-human) animal wherein the antibodies are capable of specifically binding an intact *Campylobacter jejuni* cell, the method comprising the steps of

a. providing

- 20 - a polypeptide comprising any of the sequences of SEQ ID NO:37-51, or comprising a fragment or variant thereof,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
 or
- 25 - a recombinant *Escherichia coli* or *Salmonella* cell of the invention as defined herein,

b. introducing a composition comprising said polypeptide, polynucleotide, vector or recombinant virus or recombinant cell into said animal,

c. raising antibodies in said animal,

d. isolating and optionally purifying the antibodies, and

e. selecting antibodies capable of specifically binding an intact *Campylobacter jejuni* cell.

The above methods are preferably done in a transgenic animal which can produce human antibodies.

35

PB14 DK00

21

Monoclonal/polyclonal antibodies

Antibodies of the invention may be polyclonal antibodies or monoclonal antibodies or mixtures of monoclonal antibodies. In a preferred embodiment, the antibody is a monoclonal antibody or a fragment thereof. Monoclonal antibodies (Mab's) are antibodies wherein every antibody molecule is similar and thus recognises the same epitope. The antibody may be any kind of antibody, however, it is preferably an IgG or IgA antibody.

Monoclonal antibodies are in general produced by a hybridoma cell line. Methods of making monoclonal antibodies and antibody-synthesising hybridoma cells are well known to those skilled in the art. Antibody-producing hybridomas may for example be prepared by fusion of an antibody-producing B lymphocyte with an immortalised cell line. A monoclonal antibody can be produced by the following steps. An animal is immunised with an antigen such as a full-length polypeptide or a fragment thereof. The immunisation is typically accomplished by administering the antigen to an immunologically competent mammal in an immunologically effective amount, i.e., an amount sufficient to produce an immune response. Preferably, the mammal is a rodent such as a rabbit, rat or mouse. The mammal is then maintained on a booster schedule for a time period sufficient for the mammal to generate high affinity antibody molecules. A suspension of antibody-producing cells is removed from each immunised mammal secreting the desired antibody. After a sufficient time to generate high affinity antibodies, the animal (e.g. mouse) is sacrificed and antibody-producing lymphocytes are obtained from one or more of the lymph nodes, spleens and peripheral blood. Spleen cells are preferred, and can be mechanically separated into individual cells in a physiological medium using methods well known to one of skill in the art. The antibody-producing cells are immortalised by fusion to cells of a mouse myeloma line. Mouse lymphocytes give a high percentage of stable fusions with mouse homologous myelomas, however, rat, rabbit and frog somatic cells can also be used. Spleen cells of the desired antibody-producing animals are immortalised by fusing with myeloma cells, generally in the presence of a fusing agent such as polyethylene glycol. Any of a number of myeloma cell lines suitable as a fusion partner can be, for example, the P3-NS1/1-Ag4-1, P3-x63-Ag8.653 or Sp2/O-Ag14 myeloma lines, available from the American Type Culture Collection (ATCC), Rockville, Md.

Monoclonal antibodies can also be generated by other methods well known to those skilled in the art of recombinant DNA technology. An alternative method,

referred to as the "combinatorial antibody display" method, has been developed to identify and isolate antibody fragments having a particular specificity, and can be utilised to produce monoclonal antibodies.

A polyclonal antibody is a mixture of antibody molecules recognising a specific given antigen, hence polyclonal antibodies may recognise different epitopes within e.g. a polypeptide. In general polyclonal antibodies are purified from serum of a mammal, which previously has been immunised with the antigen. Polyclonal antibodies may for example be prepared by any of the methods described in *Antibodies: A Laboratory Manual*, By Ed Harlow and David Lane, Cold Spring Harbor Laboratory Press, 1988. Polyclonal antibodies may be derived from any suitable mammalian species, for example from mice, rats, rabbits, donkeys, goats, and sheep.

Specificity

The antibodies of the invention may be monospecific towards any of the polypeptides of SEQ ID NO:1-51. In another embodiment, the antibody is bispecific or multispecific having at least one portion being specific towards any of the polypeptides of SEQ ID NO:1-51.

Monospecific antibodies may be monovalent, i.e. having only one binding domain. For a monovalent antibody, the immunoglobulin constant domain amino-acid sequences preferably comprise the structural portions of an antibody molecule known in the art as CH1, CH2, CH3 and CH4. Preferred are those which are known in the art as C_L. Furthermore, insofar as the constant domain can be either a heavy or light chain constant domain (C_H or C_L, respectively), a variety of monovalent antibody compositions are contemplated by the present invention. For example, light chain constant domains are capable of disulphide bridging to either another light chain constant domain, or to a heavy chain constant domain. In contrast, a heavy chain constant domain can form two independent disulphide bridges, allowing for the possibility of bridging to both another heavy chain and to a light chain, or to form polymers of heavy chains. Thus, in another embodiment, the invention contemplates a composition comprising a monovalent polypeptide wherein the constant chain domain C has a cysteine residue capable of forming at least one disulphide bridge, and where the composition comprises at least two monovalent polypeptides covalently linked by said disulphide bridge.

P814 DK00

23

In another embodiment of the invention the antibody is a multivalent antibody having at least two binding domains. The binding domains may have specificity for the same ligand or for different ligands.

5 Multispecificity, including bispecificity

In a preferred embodiment the invention relates to multispecific antibodies, which have affinity for and are capable of specifically binding at least two different entities.

10 In one embodiment, the multispecific antibody is a bispecific antibody, which carries at least two different binding domains, at least one of which is of antibody origin. A bispecific molecule of the invention can also be a single chain bispecific molecule. Multispecific molecules can also be single-chain molecules or may comprise at least two single-chain molecules. The multispecific, including bispecific antibodies, may be produced by any suitable manner known to the person skilled in the art. A number of approaches have been developed such as the ones described in WO 94/09131; WO 94/13804; WO 94/13806 or U.S. Pat. Nos. 5,260,203; 5,455,030; 4,881,175; 5,132,405; 5,091,513; 5,476,786; 5,013,653; 5,258,498; and 5,482,858.

20 Using a bispecific or multispecific antibody according to the invention the invention offers several advantages as compared to monospecific/monovalent antibodies. A bispecific/multispecific antibody has a first binding domain capable of specifically recognising and binding any of the *Campylobacter jejuni* polypeptides of SEQ ID NO:1-51, whereas the other binding domain(s) may be used for other purposes. In one embodiment, at least one other binding domain is used for binding to a *Campylobacter jejuni* polypeptide, such as binding to another epitope on the same 25 *Campylobacter jejuni* polypeptide as the first binding domain. Thereby specificity for *Campylobacter jejuni* may be increased as well as increase of avidity of the antibody. In another embodiment the at least one other binding domain may be used for specifically binding a mammalian cell, such as a human cell. It is preferred that the at least other binding domain is capable of binding an immunoactive cell, such as a 30 leukocyte, a macrophage, a lymphocyte, a basophilic cell, and/or an eosinophilic cell, in order to increase the effect of the antibody in a therapeutic method. This may be accomplished by establishing that the at least one other binding domain is capable of specifically binding a mammalian protein, such as a human protein, such as a protein selected from any of the cluster differentiation proteins (CD), in particular 35 CD64 and/or CD89..

Humanised antibodies

It is not always desirable to use non-human antibodies for human therapy, since the non-human "foreign" epitopes may elicit an immune response in the individual to be treated. To eliminate or minimise the problems associated with non-human antibodies, it is desirable to engineer chimeric antibody derivatives, i.e., "humanised" antibody molecules that combine the non-human Fab variable region binding determinants with a human constant region (Fc). Such antibodies are characterised by equivalent antigen specificity and affinity of the monoclonal and polyclonal antibodies described above, and are less immunogenic when administered to humans, and therefore more likely to be tolerated by the individual to be treated.

Accordingly, in one embodiment the antibody of the invention is a humanised antibody. Humanised antibodies are in general chimeric antibodies comprising regions derived from a human antibody and regions derived from a non-human antibody, such as a rodent antibody. Humanisation (also called Reshaping or CDR-grafting) is a well-established technique for reducing the immunogenicity of monoclonal antibodies (mAbs) from xenogeneic sources (commonly rodent), increasing the homology to a human immunoglobulin, and for improving their activation of the human immune system. Thus, humanised antibodies are typically human antibodies in which some CDR residues and possibly some framework residues are substituted by residues from analogous sites in rodent antibodies.

It is important that humanised antibodies retain high affinity for the antigen and other favourable biological properties. To achieve this goal, according to a preferred method, humanised antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanised products using three-dimensional models of the parental and humanised sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of certain residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the recipient and import sequences so that the desired antibody characteristic, such as

P814 DK00

25

increased affinity for the target antigen(s), is maximised, although it is the CDR residues that directly and most substantially influence antigen binding.

One method for humanising MAbs relates to production of chimeric antibodies in which an antigen binding site comprising the complete variable domains of one antibody is fused to constant domains derived from a second antibody, preferably a human antibody. Methods for carrying out such chimerisation procedures are for example described in EP-A-0 120 694 (Celltech Limited), EP-A-0 125 023 (Genentech Inc.), EP-A-0 171 496 (Res. Dev. Corp. Japan), EP-A-0173494 (Stanford University) and EP-A-0 194 276 (Celltech Limited).

The humanised antibody of the present invention may be made by any method capable of replacing at least a portion of a CDR of a human antibody with a CDR derived from a non-human antibody. Winter describes a method which may be used to prepare the humanised antibodies of the present invention (UK Patent Application GB 2188638A), the contents of which are incorporated by reference.

As an example, the humanised antibodies of the present invention may be produced by the following process:

- (a) constructing, by conventional techniques, an expression vector containing an operon with a DNA sequence encoding an antibody heavy chain in which the CDRs and such minimal portions of the variable domain framework region that are required to retain antibody binding specificity are derived from a non-human immunoglobulin, and the remaining parts of the antibody chain are derived from a human immunoglobulin;
- (b) constructing, by conventional techniques, an expression vector containing an operon with a DNA sequence encoding a complementary antibody light chain in which the CDRs and such minimal portions of the variable domain framework region that are required to retain donor antibody binding specificity are derived from a non-human immunoglobulin, and the remaining parts of the antibody chain are derived from a human immunoglobulin;
- (c) transfected the expression vectors into a host cell by conventional techniques; and
- (d) culturing the transfected cell by conventional techniques to produce the humanised antibody.

The host cell may be co-transfected with the two vectors of the invention, the first vector containing an operon encoding a light chain derived polypeptide and the sec-

ond vector containing an operon encoding a heavy chain derived polypeptide. The two vectors contain different selectable markers, but otherwise, apart from the anti-body heavy and light chain coding sequences, are preferably identical, to ensure, as far as possible, equal expression of the heavy and light chain polypeptides. Alternatively, a single vector may be used, the vector including the sequences encoding both the light and the heavy chain polypeptides. The coding sequences for the light and heavy chains may comprise cDNA or genomic DNA or both.

The host cell used to express the altered antibody of the invention may be either a bacterial cell such as Escherichia coli, or a eukaryotic cell. In particular a mammalian cell of a well defined type for this purpose, such as a myeloma cell or a Chinese hamster ovary cell may be used.

The general methods by which the vectors of the invention may be constructed, transfection methods required to produce the host cell of the invention and culture methods required to produce the antibody of the invention from such host cells are all conventional techniques. Likewise, once produced, the humanised antibodies of the invention may be purified according to standard procedures.

Human antibodies

In a more preferred embodiment the invention relates to an antibody, wherein the binding domain is carried by a human antibody, i.e. wherein the antibodies have a greater degree of human peptide sequences than do humanised antibodies.

Human mAb antibodies directed against human proteins can be generated using transgenic mice carrying the human immune system rather than the mouse system. Splenocytes from these transgenic mice immunised with the antigen of interest are used to produce hybridomas that secrete human mAbs with specific affinities for epitopes from a human protein (see, e.g., Wood et al. International Application WO 91/00906, Kucherlapati et al. PCT publication WO 91/10741; Lonberg et al. International Application, WO 92/03918; Kay et al. International Application 92/03917; Lonberg, N. et al. 1994 Nature 368:856-859; Green, L. L. et al. 1994 Nature Genet. 7:13-21; Morrison, S. L. et al. 1994 Proc. Natl. Acad. Sci. USA 81:6851-6855; Bruggeman et al. 1993 Year Immunol 7:33-40; Tuallion et al. 1993 PNAS 90:3720-3724; Bruggeman et al. 1991 Eur J Immunol 21:1323-1326). Such transgenic mice are available from Abgenix, Inc., Fremont, Calif., and Medarex, Inc., Annandale, N.J. It has been described that the homozygous deletion of the antibody heavy-chain joining region (IH) gene in chimeric and germ-line mutant mice results

P814 DK00

27

in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, e.g., Jakobovits et al., Proc. Natl. Acad. Sci. USA 90:2551 (1993); Jakobovits et al., Nature 362:255-258 (1993); Bruggemann et al., Year in Immunol. 7:33 (1993); and Duchosal et al. Nature 355:258 (1992). Human antibodies can also be derived from phage-display libraries (Hoogenboom et al., J. Mol. Biol. 227: 381 (1992); Marks et al., J. Mol. Biol. 222:581-597 (1991); Vaughan, et al., Nature Biotech 14:309 (1996)).

Suitable methods for producing human monoclonal antibodies have furthermore been described in WO 03/017935, WO 02/100348, US 2003 091561, and US 2003 194403.

Binding fragments of antibodies

In one embodiment of the invention, the antibody is a fragment of an antibody, preferably an antigen binding fragment or a variable region. Examples of antibody fragments useful with the present invention include Fab, Fab', F(ab')₂ and Fv fragments. Papain digestion of antibodies produces two identical antigen binding fragments, called the Fab fragment, each with a single antigen binding site, and a residual "Fc" fragment, so-called for its ability to crystallise readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen binding fragments which are capable of cross-linking antigen, and a residual other fragment (which is termed pFc'). Additional fragments can include diabodies, linear antibodies, single-chain antibody molecules, and multispecific antibodies formed from antibody fragments.

The antibody fragments Fab, Fv and scFv differ from whole antibodies in that the antibody fragments carry only a single antigen-binding site. Recombinant fragments with two binding sites have been made in several ways, for example, by chemical cross-linking of cysteine residues introduced at the C-terminus of the VH of an Fv (Cumber et al., 1992), or at the C-terminus of the VL of an scFv (Pack and Pluckthun, 1992), or through the hinge cysteine residues of Fab's (Carter et al., 1992).

Preferred antibody fragments retain some or essentially all of the ability of an antibody to selectively bind with its antigen. Some preferred fragments are defined as follows:

(1) Fab is the fragment that contains a monovalent antigen-binding fragment of an antibody molecule. A Fab fragment can be produced by digestion of whole anti-

body with the enzyme papain to yield an intact light chain and a portion of one heavy chain.

5 (2) Fab' is the fragment of an antibody molecule and can be obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain. Two Fab' fragments are obtained per antibody molecule. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxyl terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region.

10 (3) (Fab')₂ is the fragment of an antibody that can be obtained by treating whole antibody with the enzyme pepsin without subsequent reduction. F(ab')₂ is a dimer of two Fab' fragments held together by two disulfide bonds.

15 (4) Fv is the minimum antibody fragment that contains a complete antigen recognition and binding site. This region consists of a dimer of one heavy and one light chain variable domain in a tight, non-covalent association ($V_H - V_L$ dimer). It is in this configuration that the three CDRs of each variable domain interact to define an antigen binding site on the surface of the $V_H - V_L$ dimer. Collectively, the six CDRs confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognise and bind antigen, although at a lower affinity

20 than the entire binding site.

In one embodiment of the present invention the antibody is a single-chain antibody, defined as a genetically engineered molecule containing the variable region of the light chain, the variable region of the heavy chain, linked by a suitable polypeptide linker as a genetically fused single chain molecule. Such single-chain antibodies are also referred to as "single-chain Fv" or "sFv" antibody fragments. Generally, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains that enables the sFv to form the desired structure for antigen binding.

30 The antibody fragments according to the invention may be produced in any suitable manner known to the person skilled in the art. Several microbial expression systems have already been developed for producing active antibody fragments, e.g. the production of Fab in various hosts, such as *E. coli* or yeast has been described. The fragments can be produced as Fab's or as Fv's, but additionally it has been shown that a V_H and a V_L can be genetically linked in either order by a flexible polypeptide linker, which combination is known as an scFv.

P814 DK00

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Compositions of the invention

In a further aspect, the invention relates to a composition comprising a carrier and an isolated polypeptide consisting of any of the sequences set forth in SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51.

5 In a even further aspect, the invention relates to a composition comprising a carrier and any one or more of

- an antibody of the invention as defined herein,
- an antigenic fragment of the invention as defined herein,
- 10 - a polynucleotide of the invention as defined herein,
- an expression vector of the invention as defined herein,
or
- a recombinant cell of the invention as defined herein.

In one embodiment, the carrier of the above compositions is water.

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In a further main aspect, the present invention relates to pharmaceutical compositions useful for practising the methods described herein. Thus, the invention relates to a pharmaceutical composition comprising a pharmaceutically-acceptable carrier and

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- an isolated polypeptide which comprises any of the sequences of SEQ ID NO:1-36, or comprises a fragment or variant of any of said sequences,
- an isolated polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide.

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- or
- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector.

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Furthermore, the invention relates to a pharmaceutical composition comprising an antibody of the invention as defined herein and a pharmaceutically-acceptable carrier.

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Pharmaceutical compositions of the present invention contain a pharmaceutically-acceptable carrier together with at least one species of polypeptide (incl. fragment and/or variant), antibody, polynucleotide, expression vector, or recombinant virus or recombinant cell as described herein, dissolved or dispersed therein as

P814 DK00

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an active ingredient. In one aspect, the invention relates to a pharmaceutical composition comprising at least one species as defined above. In other preferred embodiments, the pharmaceutical composition comprises at least two different species as defined above in order to increase the effect of the treatment.

5 As used herein, the term "pharmaceutically acceptable" used in connection with compositions or carriers represents that the materials are capable of being administered to or upon a human or animal without the production of undesirable physiological effects such as nausea, dizziness, gastric upset and the like.

10 The preparation of a pharmacological composition that contains active ingredients dissolved or dispersed therein is well understood in the art. Often such compositions are prepared as sterile injectables either as liquid solutions or suspensions, aqueous or non-aqueous, however, solid forms suitable for solution, or suspension, in liquid prior to use can also be prepared. The preparation can also be emulsified. The active ingredient can be mixed with carriers which are pharmaceutically acceptable and compatible with the active ingredient and in amounts suitable for use in the methods described herein. Suitable carriers are, for example, water, saline, dextrose, glycerol, ethanol or the like and combinations thereof. In addition, if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents and the like which enhance the effectiveness of the active ingredient.

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20 The pharmaceutical composition of the present invention can include pharmaceutically-acceptable salts of the components therein. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of the polypeptide) that are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, tartaric, mandelic and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine and the like.

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30 Pharmaceutically-acceptable carriers are well known in the art. Exemplary of liquid carriers are sterile aqueous solutions that contain no materials in addition to the active ingredients and water, or contain a buffer such as sodium phosphate at physiological pH value, physiological saline or both, such as phosphate-buffered saline. Still further, aqueous carriers can contain more than one buffer salt, as well as salts such as sodium and potassium chlorides, dextrose, propylene glycol, poly-

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P814 DK00

31

ethylene glycol and other solutes. Liquid compositions can also contain liquid phases in addition to and to the exclusion of water. Exemplary of such additional liquid phases are glycerin; vegetable oils such as cottonseed oil, organic esters such as ethyl oleate, and water-oil emulsions.

5 A pharmaceutical composition containing a polypeptide or antibody of the present invention preferably contains an amount of at least 0.1 weight percent of polypeptide or antibody per weight of total pharmaceutical composition. A weight percent is a ratio by weight of polypeptide or antibody to total composition. Thus, for example, 0.1 weight percent is 0.1 grams of polypeptide or antibody per 100 grams
10 of total composition.

15 The pharmaceutical composition may also be a kit-in-part further including an antibiotic agent, such as antibiotics selected from β -lactams, cephalosporins, penicillins, aminoglycosides, macrolide antibiotics (erythromycin, clarithromycin, or azithromycin) and fluoroquinolone antibiotics (ciprofloxacin, levofloxacin, gatifloxacin, or moxifloxacin) and/or including an immunostimulating agent, such as cytokines, interferons, growth factors, for example GCSF or GM-CSF. The kit-in-part may be used for simultaneous, sequential or separate administration.

Polypeptides of the invention

Fragments of the invention

In a main aspect, the invention relates to a fragment, preferably an antigenic fragment, of a polypeptide set forth in any of SEQ ID NO:1-51, such as a fragment of any of SEQ ID NO:1-36 or a fragment of any of SEQ ID NO:37-51. The length of such fragments may vary from 2 consecutive amino-acid residues of a polypeptide to the full-length polypeptide minus one amino-acid residue. Preferably, fragments are less than 100 consecutive amino acids, such as less than 70 or 50 consecutive amino acids, e.g. less than consecutive 40 amino acids, such as less than 30 consecutive amino acids, e.g. less than 25 consecutive amino acids, such as less than consecutive 20 amino acids in length. Thus, for example fragments can be 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19 or 20 consecutive amino acids in length. In further preferred embodiments, a fragment comprises 6 or more, such as 7 or more, e.g. 8 or more, such as 9 or more, e.g. 10 or more consecutive amino acids of the corresponding full-length sequence. Preferred ranges include fragments of between 5 and 50 consecutive amino acids in length, such as between 5 and 25 consecutive amino acids in length, e.g. between 5 and 20 consecutive amino acids

P814 DK00

32

in length. Expressed in another way, a fragment consists of a part of an amino-acid sequence which is less than 100% in length as compared to the full-length polypeptide. Preferably, the length of the fragment is less than 99%, such as less than 75%, e.g. less than 50%, such as less than 25%, e.g. less than 20%, such as less than 15%, e.g. less than 10% of the length of the full-length polypeptide. In further preferred embodiments, the fragment consists of a part of an amino-acid sequence which is less than 100%, but more than 1% in length as compared to the full-length polypeptide, such as less than 100% but more than 5%, e.g. less than 100% but more than 10%, such as less than 100% but more than 20%, e.g. less than 100% but more than 25%, such as less than 100% but more than 50% of the length of the full-length polypeptide.

Preferred specific fragments include fragments comprising one or more residues of any of the fragments of SEQ ID NO:52-119, e.g. two or more, such as three or more, e.g. four or more, such as 5 or more residues, e.g. 6 or more consecutive residues of any of the fragments of SEQ ID NO:52-119. Even more preferred specific fragments include fragments consisting of or essentially consisting of any of the sequences set forth in SEQ ID NO:52-119.

Preferably, fragments of the invention are surface-exposed in an intact *Campylobacter jejuni* cell or other cell when expressed recombinantly therein. Surface-exposure can be e.g. be determined using a monoclonal antibody specific for said fragment, e.g. as described in Singh et al. (2003) Infect. Immun. 71:3973-3946. Also preferred are fragments which are capable of inducing antibodies that can specifically bind an intact *Campylobacter jejuni* cell. This can be determined by generating monoclonal antibodies using said fragment and subsequent characterisation of the binding of individual antibodies to intact cells, e.g. as described in Singh et al. (2003) Infect. Immun. 71:3973-3946.

The full-length polypeptides of SEQ ID NO:1-51 as well as the fragments of the invention can be produced recombinantly by conventional techniques known in the art. Suitable host cells can be mammalian cells, e.g. CHO, COS or HEK293 cells. Alternatively, insect cells, bacterial cells or fungal cells can be used. Methods for heterologous expression of polynucleotide sequences in the cell types listed above and subsequent purification of the produced polypeptides, e.g. using a tag sequence

P814 DK00

33

which may be removed after purification, are well-known to those skilled in the art. Alternatively, fragments of the invention can be produced synthetically.

Variants of the invention

5 In a further main aspect, the invention relates to variants of any of the polypeptides set forth in SEQ ID NO:1-51, such as SEQ ID NO:1-36 or SEQ ID NO:37-51 or variants of fragments of any of the polypeptides set forth in SEQ ID NO:1-51.

When used herein, phrases such as 'a polypeptide having at least 95% sequence identity to SEQ ID NO:X' are used interchangeably with, and are intended to be directed to the same subject-matter as, phrases such as 'the polypeptide of SEQ ID NO:X and variants thereof, wherein the variant has at least 95% sequence identity to said sequence.'

10 Variants preferably have at least 75% sequence identity, for example at least 80% sequence identity, such as at least 85% sequence identity, for example at least 90% sequence identity, such as at least 91% sequence identity, such as at least 92% sequence identity, for example at least 93% sequence identity, such as at least 94% sequence identity, for example at least 95% sequence identity, such as at least 96% sequence identity, for example at least 97% sequence identity, such as at least 98% sequence identity, for example 99% sequence identity with the given polypeptide or fragment. Sequence identity is determined with any of the algorithms GAP, BESTFIT, or FASTA in the Wisconsin Genetics Software Package Release 7.0, using default gap weights.

15 20 25 Preferred variants of a given polypeptide or fragment are variants in which all amino-acid substitutions between the variant and the given reference polypeptide or fragment are conservative substitutions. Conservative amino-acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine, a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino-

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P814 DK00

34

acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

5 Variants of a polypeptide or of a fragment thereof also include forms of the polypeptide or fragment wherein one or more amino acids have been deleted or inserted. Preferably, less than 5, such as less than 4, e.g. less than 3, such as less than 2, e.g. only one amino acid has been inserted or deleted. 'Variants' of a polypeptide or of a fragment thereof also include forms of these polypeptides or fragments modified by post-translational modifications of the amino-acid sequence.

10 **Polynucleotides and expression vectors of the invention**

In a further aspect, the invention relates to polynucleotides, preferably isolated and/or recombinant polynucleotides, comprising a sequence encoding an antigenic fragment or variant of any of the sequences of SEQ ID NO:1-51, such as a sequence encoding an antigenic fragment or variant of any of the sequences of SEQ ID NO:1-36 or a sequence encoding a antigenic fragment or variant of any of the sequences of SEQ ID NO: 37-51.

20 Furthermore, the invention relates to expression vectors comprising a sequence encoding a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, or comprises a fragment or variant of any of said sequences. Preferred expression vectors as ones suitable for DNA vaccination. Other preferred expression vectors are ones in which a polynucleotide of the invention is under the control of a promoter that directs expression of the sequence in *Escherichia coli* or *Salmonella*. The latter expression vectors are useful in the production of a recombinant virus or recombinant cell of the invention as described herein.

25 The polynucleotides and expression vectors of the invention can be prepared by standard recombinant DNA techniques well-known to the person skilled in the art.

30 **Recombinant cells of the invention**

In a further main aspect, the invention relates to a recombinant cell transformed or transfected with a polynucleotide comprising a sequence encoding a polypeptide, said polypeptide comprising any of the sequences of SEQ ID NO:1-36, or comprising an antigenic fragment or variant of any of said sequences. Preferably, 35 said recombinant cell is an *Escherichia coli* or *Salmonella* cell, more preferably an attenuated or reduced-virulence *Escherichia* or *Salmonella* cell.

In a further aspect, the invention relates to a recombinant attenuated or reduced-virulence microbial cell, preferably an *Escherichia coli* or a *Salmonella* cell transformed or transfected with a polynucleotide comprising a sequence encoding a polypeptide, said polypeptide comprising any of the sequences of SEQ ID NO:37-51, or comprising an antigenic fragment or variant of any of said sequences.

Suitable bacterial strains for use therein have been described in e.g. Makino et al. (2001) *Microb. Pathog.* 31:1-8; Gentschev et al. (2002) *Int. J. Med. Microbiol.* 291:577-582; Turner et al. (2001) *Infect Immun.* 69:4969-4979; WO99/49026; and WO03/022307 and references therein. Examples of suitable *Salmonella* strains are CvD908-T7pol (Santiago-Machuca et al. (2002) *Plasmid* 47:108-119), ATCC 39183, ATCC 53647 and ATCC 53648. Examples of suitable *E. coli* strains are YT106 and E1392/75-2A.

Methods and uses of the invention

The products defined above can be used to treat or prevent *Campylobacter jejuni* infections, and/or disease resulting from such infections, in animals or human beings. Preferably, the animal is a chicken, duck, turkey, cow or pig. Preferred human populations are at-risk populations, such as the population of children up to 4 years old, the population of persons in industrialised nations or the population of naive or semi-immune travellers to the developing world.

Treatment and prevention herein include all types of therapeutic treatment and preventive treatment and other treatments to combat *Campylobacter jejuni*, including but not limited to vaccination, prophylaxis, active immunisation, passive immunisation, administration of antibodies, curative treatment, ameliorating treatment. In particular, passive immunisation using antibodies of the invention is a suitable treatment for immunocompromised individuals.

Thus, in a further aspect, the invention relates to a method for treatment or prevention of *Campylobacter jejuni* infection in an animal or human being comprising the step of administering any one of the following

- a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, such as any of the sequences of SEQ ID NO:1-36 or any of SEQ ID NO:37-51, or comprises a fragment or variant of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,

P814 DK00

36

- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector,
- an antibody capable of specifically binding said polypeptide,
or
- 5 - a composition as defined herein.

Preferably, said administration is done parenterally, intravenously, intramuscularly, subcutaneously, orally or intranasally.

10 Accordingly, the invention relates to

- a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, such as any of the sequences of SEQ ID NO:1-36 or any of SEQ ID NO:37-51, or comprises a fragment or variant of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- 15 - an expression vector comprising a sequence encoding said polypeptide,
- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector,
- an antibody capable of specifically binding said polypeptide,
or
- 20 - a composition as defined herein.

for use as a medicament.

Preferably, said medicament is a medicament suitable for parenteral, intravenous, intramuscular, subcutaneous, oral or intranasal administration.

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In a further aspect, the invention relates to a method for the immunisation of an animal or human being against *Campylobacter jejuni* infections comprising the step of administering

- a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, such as any of the sequences of SEQ ID NO:1-36 or any of SEQ ID NO:37-51, or comprises a fragment or variant of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
- 30 - a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector,
- 35 -

or

- a composition as defined herein.

Preferably, said administration is done parenterally, intravenously, intramuscularly, subcutaneously, orally or intranasally.

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Accordingly, in one embodiment the invention relates to use of

- a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, such as any of the sequences of SEQ ID NO:1-36 or any of SEQ ID NO:37-51, or comprises a fragment or variant of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector,

or

- a composition as defined herein,

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for the preparation of a medicament for the immunisation of an animal or human being against *Campylobacter jejuni* infections.

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Preferably, said immunisation induces a protective immune response. Preferably, 20 said medicament is a medicament suitable for parenteral, intravenous, intramuscular, subcutaneous, oral or intranasal administration.

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In a further aspect, the invention relates to the use of an antibody of the invention as defined herein for the manufacture of a medicament for the treatment or prevention of *Campylobacter jejuni* infections in an animal or human being. Thus, the invention also relates to a method for the treatment or prevention of *Campylobacter jejuni* infections comprising the step of administering an antibody of the invention as defined herein.

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Diagnostic methods of the invention

The combination of being surface-exposed and being present in relatively high copy numbers in cells also makes the 51 polypeptides identified by the inventors highly suitable as targets for detection of *Campylobacter jejuni*, allowing detection of this organism with high sensitivity.

P814 DK00

38

Accordingly, in a further main aspect, the invention relates to a method for detecting *Campylobacter jejuni* comprising the steps of

- a. providing a biological sample,
- b. contacting said sample with an indicator moiety capable of specifically binding any of the polypeptides of SEQ ID NO:1-36, and
- c. determining whether a signal has been generated by the indicator moiety.

Preferably, said indicator moiety is capable of specifically binding intact *Campylobacter jejuni* cells.

10 In another aspect, the invention relates to a method for detecting a *Campylobacter jejuni* comprising the steps of

- a. providing a biological sample.,
- b. contacting said sample with an indicator moiety capable of specifically binding any of the polypeptides of SEQ ID NO:37-51, wherein the indicator moiety furthermore is capable of specifically binding intact *Campylobacter jejuni* cells,
- 15 end
- c. determining whether a signal has been generated by the indicator moiety.

20 In preferred embodiments, a washing step is performed between the contacting step and the determination step, in order to improve the specificity of detection.

The biological sample can be faeces, urine, a tissue, tissue extract, fluid sample or body fluid sample, such as blood, plasma or serum. Another example of a biological sample is a food sample, such as a meat sample.

25 The above methods can e.g. be used to diagnose *Campylobacter jejuni* infections or campylobacteriosis in an individual. In preferred embodiments of the above methods, said indicator moiety does not pass through the outer-membrane of a *Campylobacter jejuni* cell. A preferred type of said indicator moiety is or comprises 30 an antibody, such as an antibody as defined elsewhere herein.

Those skilled in the art will understand that there are numerous well known clinical diagnostic chemistry procedures in which an indicator moiety can be used to form an binding reaction product whose amount relates to the amount of the ligand,

herein *C. jejuni* or parts thereof, in a sample. Thus, while exemplary assay methods are described herein, the invention is not so limited.

The present invention also relates to a diagnostic system, preferably in kit form, for assaying for the presence, and preferably also the amount, of *Campylobacter jejuni* in a biological sample. Methods for the preparation of diagnostic kits have e.g. been described in US 5,470,958 and references therein.

The diagnostic system includes, in an amount sufficient to perform at least one assay, an indicator moiety according to the present invention, preferably as a separately packaged reagent, and more preferably also instructions for use. Packaged refers to the use of a solid matrix or material such as glass, plastic (e.g., polyethylene, polypropylene or polycarbonate), paper, foil and the like capable of holding within fixed limits an indicator moiety of the present invention. Thus, for example, a package can be a glass vial used to contain milligram quantities of a contemplated labelled indicator moiety preparation, or it can be a microtiter plate well, to which microgram quantities of a contemplated indicator moiety has been operatively affixed, i.e., linked so as to be capable of binding a ligand.

"Instructions for use" typically include a tangible expression describing the reagent concentration or at least one assay method parameter such as the relative amounts of reagent and sample to be admixed, maintenance time periods for reagent/sample admixtures, temperature, buffer conditions and the like.

In most embodiments, the diagnostic method and system of the present invention include as a part of the indicator moiety, a label or indicating means capable of signalling the formation of a binding reaction complex containing an indicator moiety complexed with the preselected ligand (i.e. a polypeptide comprising any of the sequences of SEQ ID NO:1-51 and/or a fragment thereof). Such labels are themselves well-known in clinical diagnostic chemistry.

The labelling means can be a fluorescent labelling agent that chemically binds to antibodies or antigens without denaturing them to form a fluorochrome (dye) that is a useful immunofluorescent tracer. Suitable fluorescent labelling agents are fluorochromes such as fluorescein isocyanate (FIC), fluorescein isothiocyanate (FITC), 5-dimethylamine-1-naphthalenesulfonyl chloride (DANSC), tetramethylrhodamine isothiocyanate (TRITC), lissamine, rhodamine 8200 sulphonyl chloride (RB 200 SC). Other examples of suitable fluorescent materials include umbelliferone,

P814 DK00

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dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin and the like. A description of Immunofluorescence analysis techniques is found in DeLuca, "Immunofluorescence Analysis", in *Antibody As a Tool*, Marchalonis, et al., eds., John Wiley & Sons, Ltd., pp. 189-231 (1982).

5 Radioactive elements can be useful as labelling agents. An exemplary radiolabeling agent is a radioactive element that produces gamma ray emissions. Elements which themselves emit gamma rays, such as ^{124}I , ^{125}I , ^{128}I , ^{132}I and ^{51}Cr represent one class of gamma ray emission-producing radioactive element indicating groups. Particularly preferred is ^{125}I . Another group of useful labelling means are those elements such as ^{11}C , ^{16}F , ^{18}O and ^{13}N which themselves emit positrons, or beta emitters, such as $^{111}\text{Indium}$ or ^{3}H . Other suitable radioactive materials include ^{131}I and ^{35}S .

10 Detection using antibodies can, in other embodiments, be facilitated by coupling the antibody to another detectable substance, such as an enzyme, a prosthetic group, a luminescent materials, or a bioluminescent material. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include Streptavidin/biotin and avidin/biotin; an example of a luminescent material includes luciferin; examples of bioluminescent materials include luciferase, 20 luciferin, and aequorin.

15 In preferred embodiments, the indicating group is an enzyme, such as horseradish peroxidase (HRP) or glucose oxidase. In such cases where the principal indicating group is an enzyme such as HRP or glucose oxidase, additional reagents are required to visualise the fact that a indicator-moiety/ligand complex (immunoreactant) has formed. Such additional reagents for HRP include hydrogen peroxide and an oxidation dye precursor such as diaminobenzidine. An additional reagent useful with glucose oxidase is 2,2'-amino-di-(3-ethyl-benzthiazoline-G-sulfonic acid).

20 The linking of labels, i.e. labelling of polypeptides such as antibodies, is well known in the art. For instance, proteins can be labelled by metabolic incorporation of radioisotope-containing amino acids provided as a component in the culture medium. See, for example, Galfre et al., Meth. Enzymol., 73:3-46 (1981). The techniques of protein conjugation or coupling through activated functional groups are particularly applicable. See, for example, Aurameas, et al., Scand. J. Immunol., Vol.

8 Suppl. 7:7-23 (1978), Rodwell et al. (1984) Biotech. 3:889-894, and U.S. Pat. No. 4,493,795.

Various diagnostic assays employing the above indicator moieties can be set up to test samples for *Campylobacter jejuni*. Exemplary assays are described in detail in Antibodies: A Laboratory Manual, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press; 1988. Representative examples of such assays include: countercurrent immuno-electrophoresis (CIEP), radioimmunoassays, radioimmunoprecipitations, enzyme-linked immuno-sorbent assays (ELISA), dot blot assays, inhibition or competition assays, and sandwich assays, immunostick (dipstick) assays, simultaneous immunoassays, immunochromatographic assays, immunofiltration assays, latex bead agglutination assays, immunofluorescent assays, biosensor assays, and low-light detection assays (see e.g. also U.S. 4,376,110 and 4,486,530).

In one embodiment, the diagnostic kits of the present invention can be used in an "ELISA" format to detect the quantity of a preselected ligand in a fluid sample. "ELISA" refers to an enzyme-linked immunosorbent assay that employs an antibody or antigen bound to a solid phase and an enzyme-antigen or enzyme-antibody conjugate to detect and quantify the amount of an antigen present in a sample and is readily applicable to the present methods. Thus, in some embodiments, an indicator moiety of the present invention can be affixed to a solid matrix to form a solid support that comprises a package in the subject diagnostic systems. A reagent is typically affixed to a solid matrix by adsorption from an aqueous medium although other modes of affixation applicable to polypeptides, such as antibodies, can be used that are well known to those skilled in the art. Useful solid matrices are also well known in the art. Such materials are water insoluble and include the cross-linked dextran available under the trademark SEPHADEX from Pharmacia Fine Chemicals (Piscataway, N.J.); agarose; beads of polystyrene beads about 1 micron to about 5 millimetres in diameter available from Abbott Laboratories of North Chicago, Ill.; polyvinyl chloride, polystyrene, cross-linked polyacrylamide, nitrocellulose- or nylon-based webs such as sheets, strips or paddles; or tubes, plates or the wells of a microtiter plate such as those made from polystyrene or polyvinylchloride.

A further diagnostic method may utilise the multivalency of an antibody composition of one embodiment of this invention to cross-link ligands, thereby forming an aggregation of multiple ligands and polypeptides, producing a precipitable aggregate. This embodiment is comparable to the well known methods of immune precipitation. This embodiment comprises the steps of admixing a sample with

a composition comprising an antibody of this invention to form a binding admixture under binding conditions, followed by a separation step to isolate the formed binding complexes. Typically, isolation is accomplished by centrifugation or filtration to remove the aggregate from the admixture. The presence of binding complexes indicates the presence of the preselected ligand to be detected.

Binding partners and inhibitors of polypeptides of the invention
The surface-localisation of the 51 polypeptides to which this work relates makes them highly suitable as targets for binding partners, such as inhibitors. Surface-located polypeptides of a pathogenic microorganism often interact with the host organism. Thus, any type of binding partner of a surface-located polypeptide may interfere with host-pathogen interaction. Binding partners thus often antagonise the pathogenicity (virulence) of a microorganism. A binding partner may also be an inhibitor of the polypeptide it binds.

Thus, in a further main aspect, the invention relates to methods for the identification of binding partners of the surface-located polypeptides set forth in SEQ ID NO:1-51. Such methods may be biochemical or cell-based.

20 **Biochemical methods**

In a main aspect, the invention relates to a method for identifying a binding partner of any of the polypeptides of SEQ ID NO:1-36 or a fragment thereof, comprising the steps of

- a. providing any of the polypeptides of SEQ ID NO:1-36 or a fragment thereof,
- b. contacting said polypeptide or fragment with a putative binding partner, and
- c. determining whether said putative binding partner is capable of binding to said polypeptide or fragment.

In preferred embodiments of this method, the polypeptide or fragment thereof is provided immobilised on a solid support, such as e.g. a column or microtiter plate, and, after the contacting step, it is determined whether or not the putative binding partner has bound to the solid support. Immobilisation of the polypeptide or fragment thereof may be through direct binding to the solid support, or through indirect binding e.g. using a specific antibody. In preferred embodiments, a washing step is performed between the contacting step and the determination step, in order to

improve the specificity of detection. In further preferred embodiments, the putative binding partner is complexed with a detectable label. The putative partner may be labelled before the contacting takes place. Alternatively, labelling may also be performed after the contacting step. Furthermore, in some embodiments of this 5 method, immobilisation may be performed after the polypeptide or fragment thereof has been bound to the binding partner. In preferred embodiments, the method is a screening method wherein the method is repeated for a plurality of putative binding partners. Suitable methods to determine binding are well-known in the art, and several of them have been referred to elsewhere herein.

10 In another aspect, a host-derived binding partner of a polypeptide selected from the group of SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51 may be identified as follows: purified host membranes are electrophoretically separated, blotted over to a membrane and incubated with the

15 polypeptide of interest or fragment thereof. Binding can then be detected using antibodies specific for the polypeptide of interest or fragment thereof. The host binding partner to which the polypeptide or fragment thereof has bound can subsequently be identified by elution from the blot and subsequent analysis by mass spectrometry, or by any other technique known in the art.

20 If the binding partner of a surface-located polypeptide of a pathogenic organism is a host-derived molecule, then such an interaction between the surface-located polypeptide and the host may be important for the virulence of the bacterium. Compounds that interfere with the interaction of the surface-located polypeptide and the host-derived binding partner may thus be suitable for prevention 25 or treatment of *Campylobacter jejuni* infections. Accordingly, another method of the invention relates to a method of identifying an inhibitor of the interaction of any of the surface-located *Campylobacter jejuni* polypeptides of SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51, with a host-derived binding partner comprising the steps of:

- 30 a. providing any of the polypeptides of SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51, or a fragment thereof,
- b. providing a host-derived binding partner of said polypeptide (identified as described above or by any other method),
- c. contacting said polypeptide with said host-derived binding partner in the 35 absence of a putative inhibitor of said interaction,

P814 DK00

44

- d. contacting said polypeptide with said host-derived binding partner in the presence of said putative inhibitor,
and
- e. determining whether the strength of the binding of said polypeptide to said host-derived binding partner resulting from step d. is reduced as compared to that resulting from step c.

5 In some embodiments, step c. and d. may be performed in two different sample compartments. In other embodiments, step d. may be performed by adding the putative inhibitor to the mixture of step c. In preferred embodiments, the method is
10 repeated for a plurality of putative inhibitors.

15 Of particular interest are binding partners that inhibit an activity of a surface-located polypeptide. Such activity may be enzymatic activity, transport activity, or any type of other biochemical or cellular activity, preferably enzymatic activity.

20 Preferred host-derived binding partners are host polypeptides and host lipids. Binding may e.g. be determined as described by Szymanski and Armstrong (1996) Infect. Immun. 64:3467-3474.

25 In preferred embodiments of the above described biochemical methods, the binding between the binding partner and the surface-located polypeptide or fragment thereof has a dissociation constant or Kd less than 5×10^{-6} M, such as less than 10^{-6} M, e.g. less than 5×10^{-7} M, such as less than 10^{-7} M, e.g. less than 5×10^{-8} M, such as less than 10^{-8} M; e.g. less than 5×10^{-9} M, such as less than 10^{-9} M, e.g. less than 5×10^{-10} M, such as less than 10^{-10} M, e.g. less than 5×10^{-11} M, such as less than 10^{-11} M, e.g. less than 5×10^{-12} M, such as less than 10^{-12} M. Dissociation constants can e.g. be determined by surface plasmon resonance analysis.

Cell-based methods

30 Reducing the level of a surface-located polypeptide, by deletion or disruption of the structural gene for it or by down-regulating gene expression (see below), may affect a bacterial cell. The cell may become more sensitive to cytotoxic compounds. Especially for surface-located polypeptides, a reduction of their level may affect the function of the cell's exterior parts, such as the outer membrane or cell wall, in preventing compounds of entering the cell. Thus, reduction of the level of an

surface-located polypeptide can make a cell more 'permeable' for various compounds.

Thus, an aspect of the present invention relates to a method for identifying a compound with antibacterial activity against *Campylobacter jejuni* comprising the steps of

- a. providing a sensitised cell which has a reduced level of any of the polypeptides of SEQ ID NO:1-36, and
- b. determining the sensitivity of said cell to a putative antibacterial compound, for instance by a growth assay.

Preferably, the method is a screening method wherein the procedure is repeated for a plurality of putative antibacterial compounds. Preferred putative antibacterial compounds are ones that do not pass through the outer membrane of a *Campylobacter jejuni* cell.

Furthermore, the invention relates to a method for identifying a compound with antibacterial activity against *Campylobacter jejuni* comprising the steps of

- a- providing a sensitised cell which has a reduced level of any of the polypeptides of SEQ ID NO:37-51, and
- b. determining the sensitivity of said cell to a putative antibacterial compound, for instance by a growth assay, wherein the putative antibacterial compound is not capable of passing through the outer membrane of a *Campylobacter jejuni* cell.

Preferably, the method is screening method wherein the procedure is repeated for a plurality of putative antibacterial compounds.

The rationale behind this approach is that a cell with a lower level of the surface-located polypeptide will exhibit increased sensitivity to cytotoxic compounds, allowing identification of antibacterial compounds with low potency that are missed when using wild-type cells for the assay. Compounds identified by this method will be often need to be modified in order to improve potency. This can be done by chemical modification.

Inhibition of the activity of a surface-located polypeptide may affect the viability (i.e. survival, growth and/or proliferation) of the bacterium. Of particular interest is inhibition of surface-located polypeptides that are essential for viability of *Campylobacter jejuni*. Essentiality of a *Campylobacter jejuni* gene may e.g. be

P814 DK00

46

investigated as described in WO 02/077183. Inhibitors of essential surface-located polypeptides may not need to enter the bacterial cell to be able to affect its viability. Thus, generally fewer requirements are posed on the structure of an inhibitor of an essential surface-located target polypeptide than on an inhibitor of an intracellular target, to be effective as an antibacterial agent.

Accordingly, the invention relates to a method for finding an inhibitor of any of the polypeptides of SEQ ID NO:1-36 comprising the steps of

- a. providing two cells which differ in the level of any of the polypeptides of SEQ ID NO:1-36,
- b. determining the sensitivity of said cells to a putative inhibitor, for instance by a growth assay, and
- c. determining whether said two cells are differently affected by the presence of said putative inhibitor.

Preferably, the method is repeated for a plurality of putative inhibitors. Preferred inhibitors are ones that do not pass through the outer membrane of a *Campylobacter jejuni* cell.

Furthermore, the invention relates to a method for finding an inhibitor of any of the polypeptides of SEQ ID NO:37-51 comprising the steps of

- a. providing two cells which differ in the level of any of the polypeptides of SEQ ID NO:37-51,
- b. determining the sensitivity of said cells to a putative inhibitor, for instance by a growth assay, wherein the putative inhibitor is not capable of passing through the outermembrane of a *Campylobacter jejuni* cell, and
- c. determining whether said two cells are differently affected by the presence of said putative inhibitor.

Preferably, the method is repeated for a plurality of putative inhibitors.

The rationale behind this approach is that the viability of a cell with a lower activity of the essential polypeptide will be more affected by an inhibitor of the polypeptide than the viability of the cell with a higher level. If the two cells are differently affected, this is an indication that the inhibitor acts on the target or at least in the same biochemical pathway.

P814 DK00

47

In some embodiments of the method, the two cells with different activity of the polypeptide of interest are a wild-type cell (or other cell with wild-type activity of the gene of interest) and a sensitised cell with a reduced activity of the polypeptide of interest. In some embodiments, the different or reduced level in the sensitised cell can be a different or reduced expression level of the gene of interest (resulting in a different or reduced copy number of the polypeptide). This can be accomplished by putting the gene under control of a regulatable promoter or by regulatable expression of an antisense RNA which inhibits translation of an mRNA encoding the essential polypeptide. In other embodiments, the different or reduced activity can be a different or reduced activity of the polypeptide of interest, e.g. due to a mutation, such as a temperature-sensitive mutation.

Suitable ways of generating sensitised cells and of using these in screening for inhibitors have been described in WO 02/077183. Sensitised cells may be obtained by growing a conditional-expression *C. jejuni* mutant strain in the presence of a concentration of inducer or repressor or other conditions which provide a level of a gene product required for bacterial viability such that the presence or absence of its function becomes a rate-determining step for viability. Regulatable promoters for *Campylobacter jejuni* have e.g. been described in Kelana et al. (2003) J Food Prot 66:1190-1197 and Dedieu et al. (2002) Appl Environ. Microbiol. 68:4209-4215. The sub-lethal expression of the target gene may be such that growth inhibition is at least about 10%, such as at least about 25%, e.g. at least about 50%, such as at least about 75%, e.g. at least 90%, such as at least 95%.

In another embodiment of the cell-based assays of the present invention, sensitised cells are obtained by reduction of the level activity of a polypeptide required for bacterial viability using a mutation, such as a temperature-sensitive mutation, in the polypeptide. Growing such cells at an intermediate temperature between the permissive and restrictive temperatures produces cells with reduced activity of the gene product. It will be appreciated that the above method may be performed with any mutation which reduces but does not eliminate the activity or level of the gene product which is required for bacterial viability. This approach may also be combined with the conditional-expression approach. In this combined approach, cells are created in which there is a temperature-sensitive mutation in the gene of interest and in which this gene is also conditionally-expressed.

When screening for inhibitors of an essential polypeptide, growth inhibition can be measured by directly comparing the amount of growth, measured by the optical density of the culture relative to uninoculated growth medium, in an experimental sample with that of a control sample. Alternative methods for assaying cell proliferation include measuring green fluorescent protein (GFP) reporter construct emissions, various enzymatic activity assays, and other methods well known in the art. Other parameters used to measure viability include e.g. colony forming units. The above method may be performed in solid phase, liquid phase, a combination of the two preceding media; or *in vivo*. Multiple compounds may be transferred to agar plates and simultaneously tested using automated and semi-automated equipment.

Cell-based assays of the present invention are capable of detecting compounds exhibiting low or moderate potency against the target molecule of interest because such compounds are substantially more potent on sensitised cells than on non-sensitised cells. The effect may be such that a test compound may be two to several times more potent, e.g. at least 10 times more potent, such as at least 20 times more potent, e.g. at least 50 times more potent, such as at least 100 times more potent, e.g. at least 1000 times more potent, or even more than 1000 times more potent when tested on the sensitised cells as compared to non-sensitised cells.

A mutant *Campylobacter jejuni* strain that overexpresses a surface-located polypeptide can also be used to identify a compound that inhibits such a polypeptide. If the compound is cytotoxic, overexpression of the target polypeptide can make cells more resistant. Thus, the Invention also relates to a method for finding an inhibitor of any of the surface-located *Campylobacter jejuni* polypeptides of SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51 comprising the steps of

- a. providing two cells which differ in the activity of any of the surface-located *Campylobacter jejuni* polypeptides of SEQ ID NO:1-51, such as any of SEQ ID NO:1-36 or any of SEQ ID NO:37-51, wherein one cell contains a substantially wild-type copy number of said polypeptide and the other cell contains higher than wild-type copy number of said polypeptide,
- b. determining the sensitivity of said cells to a putative inhibitor, for instance by a growth assay, and

c. determining whether or not said two cells are differently affected by the presence of said putative inhibitor.

Overexpression may be achieved using strong promoters or by introducing multiple copies of the structural gene for a surface-located polypeptide. Strong 5 Campylobacter jejuni promoters have been described by Wosten et al. (1998) J. Bacteriol. 180:594-599. As also overexpression of polypeptides that are not the cellular target of an inhibitor can make cells resistance to an inhibitor, inhibition of the target polypeptide of interest by a putative inhibitor will need to be verified by other means, such as e.g. a biochemical assay.

10 In addition to inhibitors of a biochemical or other cellular activity of a surface-located polypeptide, the cellular methods described above can be used to identify compounds that reduce the expression level of a target, and thereby its copy number, e.g. by interfering with gene regulation.

15 In preferred embodiments of the any of the cell-based- or biochemical methods for finding binding partners or inhibitors, the method is repeated for a plurality of candidate compounds.

In a further aspect, the invention relates to the mutant Campylobacter jejuni strains 20 used in the cell-based methods described herein, such as strains in which the gene encoding the surface-located polypeptide is placed under the control of a heterologous regulatable promoter, strains carrying temperature-sensitive alleles of the surface-located polypeptides, and strains overexpressing the surface-located polypeptides.

25 Other methods of interfering with bacterial growth by targeting surface-located polypeptides, such as any of the polypeptides of SEQ ID NO:1-36 include suppression of gene expression using specific antisense molecules, such antisense RNA or DNA, and using ribozyme molecules specific for mRNA encoding the 30 essential surface-located polypeptides.

P814 DK00

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Examples**Strategy:**

The experimental steps in the project as follows: Isolate surface proteins by low pH elution. Analyse by 2-D gels and mass spectrometry. Clone into *E. coli* expression vector. Produce recombinant protein, immunise mice, challenge the immunised mice with *Campylobacter jejuni* and look for protection against disease and intestinal colonisation. *E. coli* and *Salmonella* surface localisation is also assessed (if positive, there is potential for use in attenuated vector strains).

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Bacterial culture:

Campylobacter jejuni (C.j.) strain 0:19 (CCUG 10950), a clinical isolate from human faeces was obtained from the Culture Collection, University of Goteborg (CCUG) in Sweden. It was routinely grown on blood agar plates at 37°C in atmosphere of 10% CO₂, 5% O₂.

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25**Surface proteins extraction:**

Bacteria were grown overnight on blood agar plates, harvested into 50 mM Tris pH7.8 and pelleted by centrifugation at 6000g for 5 minutes. The pellet was resuspended in 0.2 M glycine pH2.2 and the bacterial suspension was gently mixed at room temperature for 10 minutes. Bacteria were pelleted again by centrifugation at 6000g for 5 minutes, supernatant containing surface proteins was collected, neutralised with NaOH and frozen at -80°C. The sample was desalting on Amersham HiTrap desalting column before 2-D gel electrophoresis.

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35**2-D gel electrophoresis:**

Two-dimensional gel electrophoresis was performed either on the Etan Dalt 2 system (Amersham Biosciences) or on the Novex NuPage system (Invitrogen) according to the manual provided with the gel system.

In brief: First dimension runs were performed on either 7 cm or 24 cm pre-cast IPG strips (pH range 3-10 or 6-11) using the Etan IPGphor Isoelectric focusing system (Amersham Biosciences) according to the manufacturer's instructions. Isofocusing was performed at the following conditions: 7 cm pH 3-10 strips: 8000 Vh, 7 cm pH 6-11 strips: 16000Vh, 24 cm pH 3-10 strips: 52000Vh. The second dimension was performed using pre-cast 12.5 % gels (Amersham Biosciences) at 5W per gel for 15

min then total 170 W for 4-6 hours for 24 cm strips. The 7 cm strips were run on the Novex NuPage system (Invitrogen) using pre-cast 4-12% gels (Invitrogen) at 200 volts for 40 minutes. Gels were silver stained according to a modified method described originally by Mortz et al. (2001) Proteomics 1(11), 1359-1363, and spots for mass spec analysis were picked using the Ettan Spot Picker from Amersham according to the manufacturer instructions.

Mass Spectrometry:

Specific protein spots were spot-picked, and placed in Milli-Q water. These gel plugs were washed in 50 mM NH₄HCO₃ / 50% ethanol and dehydrated by incubation in 96% ethanol. Reduction and alkylation was performed by incubating in reducing solution (10 mM DTT, 50 mM NH₄HCO₃) at 56°C followed by a room temperature incubation in alkylation solution (55 mM iodoacetamide, 50 mM NH₄HCO₃) in the dark. Two cycles of washing and dehydration were then performed prior to the addition of 5 µl trypsin solution (12.5 ng/µl Promega trypsin in 50 mM NH₄HCO₃, 10% Acetonitrile). Then an additional amount of sodium bicarbonate solution was added and the digests were incubated overnight at 37°C. Trifluoroacetic acid was added to the overnight digest followed by incubation with shaking.

Parts of the extract were used in MALDI-TOF peptide mass fingerprint analysis (Reflex IV, Bruker Daltonics, Germany) and the peaklist was used in database searching against a specific *Campylobacter jejuni* database. The Mascot search program and scoring algorithm (Matrix Science, UK) was used in database searching. Peptide mass tolerance was set to 60 ppm and 0.5 Da, respectively. Search parameters were adjusted to include oxidation of Met, the addition of Carbamidomethyl groups to Cys, and trypsin was allowed to miss one cleavage site per peptide.

The fragments given in list 1 (see below) were identified. In total 51 different *Campylobacter jejuni* proteins were identified using this procedure. The full-length sequences of these proteins are given in SEQ ID NO:1-51. The proteins in the sequence listing are functionally classified according to the classification from the Sanger Institute. All proteins which were predicted from genomic sequence but had not been characterised before, and did not have any homology to previously characterised proteins, were classified as hypothetical by the Sanger Institute. Those which had homology to known proteins were named as the corresponding known protein with the pre-fix "probable" or "putative", depending on the degree of

PB14 DK00

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homology. Some proteins have small motifs, which did not allow to assign a precise biochemical/metabolic function to them, but did allow to state the fact that they possess of a certain feature, such as nucleotide binding motifs, membrane attachment sites, etc. Putative periplasmic proteins were classified as such on a similar basis – 5 they possess a short (4-6 amino acids) N-terminal motif, which may mediate transport to the periplasm.

Bioinformatic studies:

Antigenicity index studies were performed using the default parameters determined 10 using Lasergene sequence analysis software from the company DNASTar (Burland, TG (2000) Methods Mol. Biol. 132:71-91). The sequences set forth in SEQ ID NO:52-119 are predicted to be particularly antigenic fragments of their corresponding full-length polypeptides.

15 Cloning and expression in *E. coli*:

Genes corresponding to the proteins of interest were PCR amplified, operately linked to a His-tag, and the resulting construct was cloned into an *E. coli* expression vector comprising an IPTG-inducible promoter. Resulting plasmids were transformed into *E. coli* BL21(DE3) strain and protein expression was induced with 0.5 mM IPTG. Glycine eluate was prepared as above and analysed for the presence of 20 the recombinant *Campylobacter jejuni* protein by three independent methods: Coomassie staining, Western blotting with anti-his tag antibody, and mass spec analysis. Recombinant protein was purified from cultures induced overnight using NTA-Ni agarose (Qiagen) according to the manufacturer's instructions. For eight 25 transformed *E. coli* strains (the ones expressing Cj0092, Cj0143c, Cj0420, Cj0715, Cj0772c, Cj1018c, Cj1380 and Cj1643) surface-localisation was determined out as described above. All eight proteins were found on the cell-surface of *E. coli*.

Mouse immunisation and challenge:

30 Mice are immunised with recombinant protein subcutaneously 3 times (day 0, 14, 28). The antibody-response is monitored in blood and gastrointestinal secretion 7 days after each immunisation. On day 42, mice are challenged intranasally with 10^9 cfu *C. jejuni* prepared as below. Mice are observed for weight loss and clinical signs of illness for 5-7 days. Several organs are analysed for *C. jejuni* infection.

P814 DK00

53

For colonisation studies, at approximately 4-5 weeks post-vaccination, mice are challenged orally with 10^8 cfu *C. jejuni* and fecal shedding of *Campylobacter jejuni* is monitored for 14-21 days. Animals are considered colonisation negative if *C. jejuni* is not detected in three consecutive fecal samples.

5 *C. jejuni* for challenge is grown o/n on blood plates at 42°C, harvested into BHI/1%YE and diluted to OD 0.05. 75 cm² flasks containing 20 ml of BHI agar are seeded with 25 ml of this starter culture and grown o/n at 42°C. Bacteria are harvested by centrifugation, washed in PBS and finally resuspended in sterile PBS to the desired density.

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Results:

Sixteen mice per antigen (SEQ ID NO:1 (Cj0092), SEQ ID NO:8 (Cj0143c), SEQ ID NO:43 (Cj0420) and SEQ ID NO:46 (Cj0772c)) were immunised with 1µg, 5µg, 10µg or 25µg of corresponding recombinant protein (4 animals for each dose). A blood sample of 200 µl blood ml was drawn from the retro orbital plexus at day 7, left for 1 hour to coagulate, centrifuged for 10 min at 3500 G, and serum was collected. Immune response was assessed by performing Western blot analysis using purified recombinant protein and dilutions of above serum samples (see figure 1). The following specific antibody titres were obtained: at least 1:100 for SEQ ID NO:1, at least 1:50 for SEQ ID NO:8, at least 1:4 for SEQ ID NO:43 and at least 1:50 for SEQ ID NO:46. In another experiment, antibody against Cj0092 (SEQ ID NO:1) from two animals was further diluted: 1:50, 1:50, 1:100, 1:200, 1:400, 1:800, 1:1600, 1:3200, and 1:6400. 100ng of purified Cj0092 antigen was loaded on the gel, blotted and probed with the different dilutions of mouse anti-Cj0092 antibody. The antigen could be seen in all dilutions of the antibodies (figure 2).

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Salmonella surface localisation studies:

An attenuated *Salmonella* strain carrying the T7 polymerase gene is transformed with a plasmid suitable for expression of *Campylobacter jejuni* genes in this organism. Surface localisation is assayed as above.

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Immunisation with whole cell vaccine:

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E. coli and/or *Salmonella* strains carrying the protein of interest on the surface are used in immunisation studies, as both killed and live vaccines.

P814 DK00

54

List 1: Fragments of surface-located C. jejuni polypeptides

=====

Sequence: AnrP544820

5 AKVEKPLNR
DILKECGIK
DIPLVNGYPLR
GEMKIIIESMPIR
GTQWGYGAVACGR
10 GYYEIWAR
IHDGEKMEGSYK
IIIESMPIR
LNGEETSPISR
LVCGGYPASTSGK
15 NDAVYIGYYGIDTK
NNGLPPSLETIK
NNGLPPSLETIKER
SYTIEDLK
SYTIEDLKK
20 TYTYALTVECGGNGR
VEKPLNR
VPVNPVKPGDPNYK

=====

Sequence: AnrP372217

25 ALFEHGTK
ARVLLMLALT
IQEYFLK
30 IQEYFLKY
KIQEYFLK
LGFISAEDLNPQK
LGFISAEDLNPQKAR
LTSLPKVDILYSVSNDSGVAAK
35 NAPFDVSK
NAPFDVSKLTSLPK
NQKDVLK
THSLNVDAFSSPDFGDLGYIVDGK
VDILYSVSNDSGVAAK
40 VFFYNNVIK
VLLMLALT
VVVSSRVVAGCVAVSDSDEK

=====

Sequence: AnrP501075

45 EGVEYFKELSK
KLFEENCVACHGER
LEGDFFAK
LFEENCVACHGER
50 MNFPNRPADPVR
MPITTENR
NLSINDVPK
RFVQEWPNK
YGIELLSK

=====

Sequence: AnrP630851

AISEYLPK

P814 DK00

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AISEYLPKDTK
 ALKDLGIIDTNSLSEDR
 AMLNLQSEFIR
 DGKTFYTGK
 5 DLGIDTNSLSEDR
 DLGIDTNSLSEDRK
 DTKGFLNEYGIR
 EFDELPK
 EFDELPKGDK
 10 ETALTMADAALIEFINTNLSLKDER
 FYSYENLANTNEALNSK
 GDKVVDQILINK
 GEYDVGVVAVISNK
 GPLNEYGTR
 15 IQNYEADNSTNAK
 KTNILEDTR
 KWSYTSENGIEHVGAVR
 LTQLAGAQOLDK
 LTQLAGAQOLDKALK
 20 LVYDENGAPIILSYGNWGYVADPSNAK
 QLAKDIMALAR
 QSINVNDSSSTQEQTQNITNIIDKVNSK
 QSINVNDSSSTQEQTQNITNIIDKVNSK
 SIEDFFEEFADNPGLIEYGITK
 25 STVAVNDTDPQFAQALQNAYQK
 TLLKQEFLNK
 TMTNAIGSMSGLVPVQTIVTQR
 TNILEDTR
 TNILEDRAK
 30 TTGDTYEEETIK
 WSVTSENGIEHVGAVR
 ======
 Sequence: Anr P666574

35 ADTYEINSVEQDANGK
 DANYQTQEGGGVNLF
 DNSLSANETALK
 EDAINNAAIEAIGK
 ENTGRVESK
 40 FSNTLSMK
 FSNTLSMKVNWK
 FSYAKITEGSVK
 GIGSALQQK
 GRADTYEINSVEQDANGK
 45 IAGDILNATYPLK
 IIISDLLQSR
 KFNVLDR
 MSGVSINSLK
 MSGVSINSLKK
 50 RGIGSALQQK
 SGDAASDEVYKLK
 SITVFDSTPDAAK
 SITVFDSTPDAAKR
 SKTEIEVIVDVR
 55 SNTSVSTDNSGSNIQDNYSEQISK
 SSTGEGTGLTR
 SSTGEGTGLTREDAINNAAIEAIGK
 TELEVIVDVR
 TGSIEITR

PB14 DK00

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TGSIEITRTSPK
TSNLTGKSK
VBSKTGSTEITR
5 VGDICRPLSNTGSGNGYTIGR
VIKDTYTK
VNLDKDSL SANETALK
YOAPGLSADNRR
YTANVTIPK
=====

10 Sequence: AnrP758295

ADEISSIONK
ADEISSIONK
AIDALVPIGR
15 AIDALVPIGRGQR
AINEFKANHL
ALDSOLEEK
ALDSOLEEKLAK
ATKVSGTLR
20 DNAIGHALIVYDDL SK
EAYPGDVFYLSR
EAYPGDVFYLSRLLER
ELIIGDRQTGK
ELQAFQFASDLDEASR
25 ELQAFQFASDLDEASRK
EMSLILR
ERIENFDLNLEIEETGK
FKADEISSIONK
GEGLKEGASVK
30 GFLDDIAVSR
GFLDDIAVSRIK
GMALNLEESSVGIVILGK
GQGVICIIYVAIGQK
GORMVELLK
35 GVINANEYR
GVINANEYRFVEEK
HALIVYDDL SK
HALIVYDDL SKHAVAYR
HPDIFEQIR
40 IENFDLNLEIEETGK
IENFDLNLEIEETGKIIISVADGVAK
IIISVADGVAK
IIISVADGVAKVYGLK
IKEFEDGIYPFIEAK
45 KALDSOLEEK
KSVHEPLHTGK
LAKAINEFK
LDLAQYR
LLKVPVGAEALIGR
50 NIMAGEMVEFENGDK
QLERGQR
QPPYSPLSVEK
QPPYSPLSVEKQVVLIFAGTK
QSTVAQVVK
55 QTGKTTVAVDTIISQR
QVSGTLRLDLAQYR
QVVLIFAGTK
QVVLIFAGTKGPLDDIAVSR
RPPGREAYPGDVFYLSR

P814 DK00

57

SVHEPLHTGIK
 TTVAVDTIISQR
 VPVGEALIGR
 5 VPVGEALIGRVVNALGEPIDAK
 VVNALGEPIDAK
 VVNALGEPIDAKGVINANEYR
 VYGLKQNIIMAGEMVEFENGDK

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Sequenca: AnrP732169

10 AEALGAPISVPVGK
 AIAEKGTIYPAVDPLDSTS
 DEMGLDVLMFIDNIFR
 DPPAFEDQSTK
 15 DPPAFEDQSTKSEIFETGIK
 EGNDLYNEMK
 EGNDLYNEMKESNVLDK
 ESNVLDKVALCYGQMNEPPGAR
 FLSQPFFVAEVFTGSPGK
 20 FSQSGSEMSALLGR
 GIYPAVDPLDSTS
 GLKAEALGAPISVPVGK
 GVQSVLQK
 HSGYSVIFAGVGER
 25 IALTGLTMAEYFR
 IFNVTGDLIDEGEEISFDKK
 IPSAVGYQPTLASEMGK
 LVLEVA AHLGDNR
 LVVERAR
 30 MLDPNIIGEEHYK
 MLDPNIIGEEHYKVAR
 SEIFETGIK
 TTAMDMTDGLVR
 TREGNDLYNEMK
 35 VALCYGQMNEPPGAR
 VGLFGGAGVGK
 VRTIAMDMTDGLVR
 VVDLLAPYAK
 WAIHRDPFAEDQSTK
 40 YDHLPENAFYMVGNIIDEAIAK
 YISLEDTIAGFK

=====

Sequence: AnrP511634

45 DFLVYSSR
 DNSNLSDENLKK
 DQPDVLYDLNTK
 EPNQAGVFNTIYLMINSNDYIR
 EQTLFYTTAYDHDKPTLYR
 50 FSSDGGGSIVFIK
 IIVKDNNSNLSDENLK
 ILSSGGMVVASDVNVDGSK
 KSQIIMADYTLTYQK
 55 LGYPNIFMQDLNSNSAEQVVFHGR
 LLVTMAPK
 LLVIMAPKDQPDVLYDLNTK
 NGNTLSSLNVK
 NLTOLTNYSGIDVNGNFIGSDDSK
 NNSAVSTYKDFLVYSSR

P814 DK00

58

QLTANGKNLFPR
 SEQTYTLNGLEQYPFLAHK
 SFYNIIVNDLK
 SQIIMADYTLLTYQK

5 TFYFPLR
 VGKIQSIDW
 VIVDGGLNLFPK
 YDLNTNK
 YLGAQSAALGVIR

10 =====
 Sequence: AnrP57234

DLQKLITLMK
 EFVVVYHPSWTYPAK

15 EFVVVYHPSWTYFAKR
 ENLIDKFLAELDSLNQIASK
 FKQNFPK
 FLAELDSLNQIASK

20 FLAELDSLNQIASKLEK
 IDHLSYDWNELLK
 IYKIDHLSYDWNELLK
 LEKSDIYFTIGLEFEK

LITLMKDK

LQVINNMQK

25 NLEQEQTSSNLVSVSIAPOAFFVK
 NLEQEQTSSNLVSVSIAPOAFFVK
 NREFVVVYHPSWTYPAK

QNFPKLQVINNMQK

30 RYNLTQIPVEILGK
 SDIYFTIGLEFEK
 TADAFSHNL

TLAKECDAK

VFTDKFK

35 VIFVQNGFPENAAK

YNLTQIPVEILGK

YNLTQIPVEILGKEPK

YPQNEONLYK

YPQNEONLYKENLDK

40 =====
 Sequence: AnrP829849

AEIFKGATGVFGSGWFWLVYNTK

AYEWALK

45 DTSGAGKDLVSIIK

EFGSLENFK

EFGSLENFKAEFIK

EGMGSVSFYANELHPVK

FYAHINWEFVAK

HHNTYVTNLMNLIK

50 HENTYVTNLMNLIKDTEFAGK
 KLPYDTNAFGDFLSAETFSYHHGK
 LEPVGTTSNAATPITEDK

LPYDTNAFGDFLSAETFSYHHGK

NARPAYLEK

55 NQKLEPVGTSNAATPITEDK

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 Sequence: AnrP550554

AEFKGEGIVMR

P814 DK00

59

	AWAKGVLENLATNPK
	DFGTFKEDQIPVSK
	DVEVGNSLGIIFPNQDNR
	EAVKIYDEVGFR
5	FAVMNTYYIGLLK
	FMEFMLSPEIQQK
	GEIVMRSATAPYSK
	GGDRDQAR
	GTHINISGIAMTK
10	GTHINISGIAMTKSSK
	GVLENLATNPK
	GVLENLATNPKGDR
	HYNADFEIIK
	HYNADFEIICK
15	IAENIKEAVK
	IIAYNKNWNLIDISK
	ILTDSNYEFPIR
	ILTDSNYEFPIRLNDVELSQTVK
	IYDEVGFR
20	KFMEFMLSPEIQQK
	LSLEGSNSPADIFITADISNLTEAK
	MKNYEDLAK
	NDVELSQTVK
	NLGLLSPVSSK
25	NPKDVEVGNSLGIIFPNQDNR
	NTNIDISKMK
	NYEDLAKAEFK
	QVFAGEAK
	RLSLEGSNSPADIFITADISNLTEAK
30	SSKNQDAAK
	TGIKVNHTQAK
	TLLASIIANDGNK
	TLLASIIANDGNKEAK
	VNHETOAKASELIK
35	YLEEFIGPAHLR
	=====
	Sequence: AnrP139712
40	AAFNTFSEK
	AAFNTFSEKEIEELK
	AENYVLEIGSK
	AFEGGKAENYVLEIGSK
	AKQLD SVNATA SVK
	ALKEGDFAK
45	ASVEVLDEK
	ASVEVLDEKLK
	DGETIAELLILSFKPEIK
	DIKVTFPK
	DSFKEEAQK
50	EEAQKSVK
	EHLENYK
	EHLENYKK
	ELTQDAEQNLFK
	ELVGEPYFEK
55	ELVGEPYFEKFDR
	ENKELVGEPYFEK
	EYGA AHLAGK
	EYGA AHLAGKDAVFK
	FADALIEK

P814 DK00

60

	FADALIEKYNFDLPK
	PATPEAIK
	FATPEAIKTK
	FDFFEGFVDDKAFEGGK
5	FDFFEGFVDDKAFEGGK GIVEQETDMQMR
	IENVDQELIQAIYFEAYR
	IGEZEKDKI
	IPELDDEMLK
10	IPELDDEMLKK
	IPSGMIKSEVENLAK
	KINGRTTARI.TLSFKPRTK
	KLEVNDQELIQAIYFEAYR
	KLIPGEEK
15	KQGALPAVK
	LEGYEKLIPEYQTPK
	LFNDIFIPK
	LHEIQELK
	LHEIQELKIPELDDEMLK
20	LIPEYQTPK
	LLPGEEKASVEVLDEK
	LTFILDELAK
	LTFILDELAKLR
	LVNDELKGK
25	MALIEEK
	MDGFRPGK
	MDGFRPGKVPVSAVLK
	QFIPGFEDGMVGMK
	QLDSVNATASVK
30	RFATPEAIK
	SAVNSALQELKK
	SEVENLAK
	SVKMDGFRPGK
	VPVSAVLKR
35	YERELTQDAEQNLFK
	YGMNPKEHLENYK
	YNFDLPK
	=====
40	Sequence: AnrP602342
	DENILTLIK
	DKGMIYGIGK
	GETNGTGVGGNAGFVIDR
	GETNGTGVGGNAGFVIDRLTHEAIK
45	GMIYGIGK
	GMIYGIGKR
	GNVMPLIDLQR.
	IDPPPETLVK
	MTPQTRYIVLR
50	NRIDPPPETLVK
	QOTQMAGPDVDQR
	RDENILTLIK
	SNEKLEQILQK
	VPSVPDYVLGVFNMR
55	=====
	Sequence: AnrP467527
	DIEPATFSTGSGALDK
	DIEPATFSTGSGALDKGK

P814 DK00

61

DIPIVFNSSLNSNEFMNEK

EDPRFK

EMMQQMGFQVVEAK

FDENIVK

5 FKDIPIVFNSSLNSNEFMNEK

FNASDFNFELAK

FTGTALILDDDSMTAR

GVQEAGGEGLVVK

GVVIFPVVNLA

10 IFKQGHDK

IIVSDVEMPQMDGFHFAAR

IPSILTELPGVPDYIEGIPDLR

KHQSSEQG

MFDENIVK

15 QGHDKVYEGIYGVNVSK

TDIDPGKIEK

TGSNEMELVDFR

VIITEFSNLLIGFIVHEAKR

VKEMMQQMGFQVVEAK

20 VYEGIYGVNVSK

=====

Sequence: AnrP311344

AIYDDDKNALIKPK

25 AMSEVKDEFLK

AVIIDAKYFSPLEQSYVITK

DKIVLGENISPVVLHVDSK

EFDLFFSADTK

EVLENLGLNELLK

30 EVLENLGLNELLKDK

ITHLSIANPK

IVLGENISPVVLHVDSK

KLAFEFNEFIGSSK

LAPEFNEFIGSSX

35 NSDIAIVAYSLVSSINHPK

QGREFDLFFSADTK

TEPEDKIELVPGASGK

VAPYGVAAK

YFSPLEQSYVITK

40 =====

Sequence: AnrP505685

ALDFTAPAVLGNNIEIVQDFNLYK

45 ALDFTAPAVLGNNIEIVQDFNLYKNIGPK

ANPKGVAEYLGK

DFTFVCPSEIIIAFDK

DFTFVCPSEIIIAFDKR

FPLVADLT

FPLVADLTQIAR

50 GAVVFFYPK

GDEGMKANPK

GIEVIGISGDNEFSHFAWK

GSFLLDADGTVR

GSFLLDADGTVRAVNDLPLGR

55 GVAEYLGK

GVAEYLGKNEAK

HAVVNDLPLGR

KALDFTAPAVLGNNIEIVQDFNLYK

MVDTMLPTNEHGEVCPAGWNK

P814 DK00

62

NFDVLYAEAVALR
 NFDVLYAEAVALRGSFLLDAQCTVR
 NIDEMRL
 NIDEMRLVDTMLFTNEHGEVCAGWNK
 5 NIGPKGAVVFFYPK
 NTPVNQGGIGQVK
 NTPVNQGGIGQVKFPLVADLTK
 QIARNFDVLYAEAVALR
 RYQEFK
 10 YQEFKNR
 ======
 Sequence: AnrP681041

AGTLADOAK
 15 ALTKEEQK
 ASEFTLEK
 ASEFTLEKAELGK
 DQKGVDIELK
 EAKSIEETFLK
 20 EMGSVQLGIK
 FANLGDFK
 FANLGDFKGDANGMVK
 FDKELEGDEK
 FLEGDEKALT
 25 GDANGMVKTPTLR
 GPIQADPEMATPAK
 GVDEILKQNGVK
 ISSLPYVSEFK
 ISSLPYVSEFKK
 30 KLYFEPR
 NSGLVALPK
 NSGLVALPKDQK
 SGIISCNTHNVGLGGTDGISTAIGHK
 SGVNFDTIADATANPER
 35 SLITGTPAIVVPQLPISTEK
 TLITPSRFDK
 ======
 Sequence: AnrP72219

40 AGLNVLSLER
 AITVGGQQGASLPHK
 ALHKFITDK
 ALNYNFTR
 AMSTGKYTIR
 45 ASPLNTVIPK
 ASPLNTVIPKAMSTGK
 CAEGILKYHK
 DAFGMPLLR
 DAFGMPLLRITYNFTDQDR
 50 DMEPYYDR
 DMEPYYDRFEK
 DTVTFRHDPSGLALPYR
 DYSVVPPYQSTHNTGGTTMGADR
 FEKTCGVSGEPNPLAEK
 55 PGCEYGAK
 FITDKTAEVAK
 FMPYDFEIQTLSK
 FVDTRTMK
 GGYTNPDGQDLAPCQYCAYCER

P814 DK00

63

GHMQSTENFNYIHDDEWR
HOPSGLALPYR
HDPGLALPYRK
KALNYNFTR
5 LLMVSNIGEQYDPK
LLMVSNIGEQYDPKTGK
LTYNFTDQDR
LTYNFTDQDRAHK
MGAFRSSSPYPQEPLENTK
10 MQGVKSIA
NNYLSLDPTYK
SSNLHTYR
SSNLHTYRLPASNPK
15 SSPYPQEPLENTKMLK
TCGVSGEPNPLAEK
TCGVSGEPNPLAEKGAFR
TYSNVTPQILK
TYSNVTOQILKK
20 VTGVKFVDTR
YGINYGLMQDCSK
YGINYGLMQDCSKDTVTFR
YGNKLGNNDYTLQDWGVTYK
=====
25 Sequence: AnrP490750

AHTDVGFK
ARTDVGFKIK
30 DIVLDAEIGGVAKCK
DNHLQQDDFFK
DNHLQQDDFFKAK
DYSAVIDFPASAEFK
DYSAVIDFPASAEFKK
EKIGFSLNGK
35 EYTLDKAHTDVGFK
GKMTGTLTIAGVSK
GNFKDYSAVIDFPASAEFK
HLOQISNVK
HLOQISNVKGNFK
40 IASVNTEENQTR
IASVNTEENQTRDNHLQQDDFEK
IGFSLNKGKIK
IKMLQISNVK
LDVTIKIASVNTEENQTR
45 MTGTLTIAGVSK
VLLSSILVAVSLLSTGLFAK
YPDMDTFTMK
YPDMDTFTMKK
=====
50 Sequence: AnrP569688

AEVISSYSK
AGEHGRGFIAVVADEVK
ATTEVEMNINLLK
55 ATTEVEMNINLLKQQNANEMYTQSEQVEK
CEVAENASLDLFNVFK
DITQHSIINK
DITQHSIINKCEVAENASLDLFNVFK
DVAGTLHR

P814 DK00

64

DVSDQTNLLALNAAIEAAR
 EIFSKSGK
 EMLDESDH
 ERFQONK
 5 PGQNKSPLK
 FGSKINHSDLQK
 FQSENLELK
 FOSENLELKNK
 FTHLVNEAHSTNSNAVGIASEAFVSLAK
 10 GFAVVADEV
 GFAVVADEVK
 IEKFQSENLELK
 INEPHEK
 INEPHEKVHENMNAITIANTEDISK
 15 INHSDLQK
 INHSDLQKLEEENK
 ISIDSNAHIMSPSEK
 ITSLEQALESK
 20 ITSLEQALESKLK
 LDHIAFK
 LEEENKNLTHK
 LGKWLASTGK
 LKTDLLNVLLTGVLK
 LNGYKEIFSK
 25 NKITSLEQALESK
 NLTHKIEK
 QLADEHTSCR
 QLADEHTCRLGK
 QNANEMYTQSEQVEK
 30 SFLKINEPHEK
 SGKQLADHTSCR
 SVDEITNVINLIK
 SVDEITNVINLIKDVSDQTNLLALNAAIEAAR
 TDLLNVLLTGVLK
 35 TQKATTEVEMNINLK
 TRDVAGTLHR
 VHENMNAITIANTEDISK
 VHENMNAITIANTEDISKDITQHSIINK
 WLASTGKER
 40 ======
 Sequence: AnRP852550
 DAEEGRTSLSMELSTLK
 DAHFDFKLPDR
 45 DELSQYLANYK
 DELSQYLANYKK
 ELMSELK
 ELMSELKCK
 GKDAHFDFK
 50 HNELDDMIK
 HNELDDMIKDAAEGR
 LFDRHNELEDDMIK
 LHEYRELMSELK
 LHVKDELSQYLANYK
 55 MLHEYR
 MLHEYRELMSELK
 TSLSMELSTLK
 TSLSMELSTLKK
 ======

PB14 DK00

65

Sequence: AnrP255677

AGIKSGDIIILK
 DFNDMCKIQTNGEFGGLGITVGMK
 5 DGALTVVSPIEGTPADK
 DGALTVVSPIEGTPADKAGIK
 DNKNLISQK
 EDKQENK
 EEQVQKR
 10 EIIKIESVYAK
 GATKPFDTVLTR
 GATKPFDTVLTRREIJK
 GRIASENQEYK
 GSVQQIIPINK
 15 GSVQQIIPINKTEALR
 GVIVGENTFGK
 GVIVGENTFGKGSVQQIIPINK
 IASENQEYK
 IASENQHYKADPK
 20 INDEATLGINLNDAVDK
 INDEATLGINLNDAVDKMR
 IQTNGEFGGLGITVGMK
 KGATKPFDTVLTR
 LEALDKLT
 25 MIENENIILYLR
 MMELILK
 NNPGGLLNQAIQLGVNLJVDK
 QENKDNK
 QHLESELEK
 30 QHLESELEKIDK
 QINDDAQLK
 QINDDAQLKSAIDTIK
 RGVIVGENTEGK
 RLEALDK
 35 SLSGLLSNLDKSSFLNEK
 TIQAVGVVKPDIEVFPK
 TQITLTIFR
 TQITLTIFRK
 VNTQEDGFSIK
 40 VNTQEDGFSIKESDLK
 VTNFDDKVVVDVASK
 YPNVKGVTLSDLR
 YYLPSSR

45 Sequence: AnrP252410

AKVNFTDGTSDIYDR
 AYKGCEGTNHGHVFFEDGTK
 CGINVDDK
 50 CGINVDDKGVPMLDENK
 DIHEAGNSGK
 DIHEAGNSGKVELK
 EFTRLNDINLK
 EHNTIEVEFGSEVESVK
 55 EHNTIEVEFGSEVESVKNENGVFLVSTAK
 ESTIETFQNALK
 EVLILEK
 EVLILEKSNNICOTIMQFYK
 GCEGTNHGHVFFEDGTK

P814 DK00

66

GCEGTNIGHVPFEDGTKESTIETFQNALK
 .GIFVAGDLATK
 GVPLMDENK
 GVPLMDENKQSNVK
 5 GVYECKNIIVAIKR
 IDLIVVGAGPTGIGCAVEAK
 IDLIVVGAGPTGIGCAVEAKLK
 INFNANSVLGN
 IYIAIGGSTPLDFLQK
 10 ILVVGGGNSAAEYAVDLANSQVSLCYR
 KIDLIVVGAGPTGIGCAVEAK
 LGIDINEVEDDNGK
 LGIDINEVEDDNGKAK
 LNDINLKDIEAGNSGK
 15 MGKPNKPDYK
 NENGVFLVSTAK
 NGASIVTGLNDAVK
 NGASIVTGLNDAVKILSVL
 NIIVAIKR
 20 NIIVAIGRMGKPNKPDYK
 NKEVLLLEK
 SNNICQTLMQFYK
 SNNICQTLMQFYKDGK
 VNFTDGTSDIYDR
 25 ======
 Sequence: AnrP916533

DTIEELVMSDVSK
 ELFLALAK
 30 IAGSSTVYPFTSFVAEEYASIK
 IGLVPLSDDKLK
 ILNDELVK
 INAANIDGVTPSEESIADEK
 INAANIDGVTPSEESTADEKYELAR
 35 IPEYKGEYK
 ISVYGPSSSGTR
 IYMSDDLAK
 KELFLALAK
 KILNDELVK
 40 KISVYGPSSSGTR
 LIPNPYTNWNQINK
 LSEFETCK
 LSEFETCKK
 QDGAYIPSGENDNLIVSK
 45 TIRODGAYIPSGENDNLIVSK
 TNAFLNITK
 TNAFLNITKK
 TPIVESLGTGGQFK
 VFCEGTTDISNASRPMK
 50 ======
 Sequence: AnrP126795

AGQSEEFKAEISK
 AGQSEEFKAEISKCR
 55 EFLKQNLK
 FFILQNLK
 IGFDLKSYK
 IGGELVYSTCTFTK
 ILLDAPCSTFAK

P814 DK00

67

ILPSLDYDGFPIAK
 INVVCYLFDAK
 INVVCYLFDAKDK
 KINVVCYLFDAK
 5 LELLDIDLENVEAK
 MQNILSSFAQEK
 MQNILSSFAQEKNVCVFANTLK
 NIGNLCPLK
 NIGNLCPLKFDK
 10 NLKNYGVMNAK
 NVCFANTLKTTSIEELEK
 QNTI.QSFAQEK
 SEFKLELLDIDLENVEAK
 TSIEELEKEPLK
 15 ======
 Sequence: AnrP327756

DAELKIEK
 DRMSVYDK
 20 EANALKTEEDIAK
 ELEEEKIK
 EQLDAANDEIVR
 EQLDAANDEIVRLDK
 GEEIVTCPHCGR
 25 GEEIVTCPHCGRILYK.
 IDEEIKDIRNQK
 IDQEIDSYEPK
 IDQEIDSYEPKIDSINK
 30 IDSINKTLK
 IEEDIAKEQLDAANDEIVR
 IEKINADLEK
 IKQEONINEIR
 ILENKETYK
 ILYKEQEEQN
 35 IQNNAHISEPSAK
 IYDKTYLSVVK
 KELEEEK
 KQACYGCFMK
 LDKILENK
 40 LVSEMNQK
 MNKYLEQLVLLSK
 MSVYDKK
 NKYLEQLVLLSK
 NTAVVPVKK
 45 QACYGCFMK
 QEQQNINEIR
 QEQQNINEIRVSIK
 SEMEVLEK
 SEMEVLEKDR
 50 SGVVKTEK
 TEKEANALK
 TKLVSEMNQK
 TLKDAELK
 TYLSVVKGEEIVTCPHCGR
 55 VLSFYEK
 VLSFYEKIR
 VSIKSEMEVLEK
 WAKNTAVVPVK
 YLEQLVLLSK

P814 DK00

68

=====

Sequence: AnrP684299

5 AENRAFGIYK
 AFGIYKLK
 DQKHYHVPITLSPFGYSTYR
 DYYTSHK
 FFTKEYYTSHK
 HYHVPITLSPFGYSTYR
10 IGDLLPYEK
 IGDLLPYEKAENR
 INTFYPFVEVSFELSK
 KVSBEFTTEENGR
 LEANQQWK
15 LEANQQWKK
 VKVELYK
 VSEEFTEENGR
 VSEEFTEBENGRIGDLLPYEK
=====

20 Sequence: AnrP586832

AFNKDLNK
AKFEGMIDSLVAETITK
ALDDDLRBTLK
25 ALSEVSHK
 ALSEVSHKLAENMYK
 ATKEAGTIAGLNVLR
 DAELHKEEDK
 DDDVIDAEVE
30 DEIKEIVMVGGSTR
 DEPNNTANDK
 DEPNNTANDKK
 DETGIDLK
 DETGIDLKNDVMALQR
35 DNKSLGNFNLEGIPPAPR
 DVLLLDVTPLSLGIETLGGVMTK
 EAGTIAGLNVLRIINEPTSAALAYGLDK
 EAVDARNAADSLAHQVEK
40 EEIESKMK
 EFSRDNK
 EGKNTTPSVVAFTDK
 EIVMVGGSTR
 EIVMVGGSTRVPLVQEEVK
45 ELSSANETEINLPFITADASGPK
 ENIQKALDDLK
 EQVFSTAEDNQSAVTINVQGER
 EQVFSTAEDNQSAVTINVQGEREFSR
 FEGMIDSLVAETITK
50 GDVKDVLLLDVTPLSLGIETLGGVMTK
 GESKVIPNK
 GEVLVGDSAK
 GEVLVGDGSAKR
 GMPQIEVTFDIDANGILTVSAK
55 GTTIPTKK
 IINEPTSAALAYGLDK
 IINEPTSAALAYGLDKK
 IMGLMINEDAEEK
 IMGLMINEDAEEK

P814 DK00

69

INEVVSDAGLK
 INEVVSDAGLKK
 ITGSSGLSEEEINNMVK
 ITGSSGLSEEEINNMVKDAELHK
 5 IYTPQEISAK
 KELSSANETEINLPFITADASGPK
 KEQVFSTAEDNQSavitinVLQGER
 LAENMYK
 LAENMYKK
 10 LIDFLANEFK
 LIDFLANEFKDETGIDLK
 LKEAAENAK
 LPYHITER
 15 LPYHITERNGACAIELAGK
 MKALSEVSHK
 MSKVIGIDLGTTNSCVAVYER
 NAADSLAHQVEK
 NAADSLAHQVEKSLSELGEK
 20 NDVMALQR
 NDVMALQRK
 NGACAIELAGK
 NGACAIELAGKITYTPQEISAK
 NQNASKEEIESK
 NRLPYHITER
 25 NTTPSVVAFTDK
 NTTPSVVAFTDKGEVLVGDSAK
 QAVTNPEK
 RIMGLMINEDA
 RQAVTNPEK
 30 SKVIGIDLGTTNSCVAVYER
 SLGNFNLEGIPPAPR
 SLSLSELGEK
 SLSLSELGEKVAADK
 SVNPDEVVAIGAAIQGAVIK
 35 TIYSIKR
 VAAADKENTQK
 VIGIDLGTTNSCVAVYER
 VIGIDLGTTNSCVAVVERGESK
 VIPNKEGK
 40 VPLVQEEVK
 VPLVQEEVKR
 ======
 Sequence: AnrP524051
 45 AIINEHYK
 AIINEHYKDILIPAF
 AKLIELNK
 ALDDVDIALINSNFALGAGLNPSK
 ALEEKELDANLYQHKPFLEEYNLK
 50 ALELLLEKAK
 DTIFREOK
 EDKNSPYVNYYVVR
 ELDANLYQHKPFLEEYNLK
 ELDANLYQHKPFLEEYNLKK
 55 FKAIINEHYK
 GSNLIATTPVLIAPVGVYSK
 GSNLIATTPVLIAPVGVYSKK
 IKNLENLK
 IVEFSDYILPNR

P814 DK00

70

LIELNKNTLK
LKFIELD
NKGYELK
NLENLKEGAR
5 NSPYVNYVVVR
NTLKTPFLDINK
TKVIDEILR
TPLDINKNPK
VAIPNDATNESR
10 VIDEILR

Sequence: AnrP579672

15 ALDIIAKK
ALKTPLDIIDNPK
ALNDVDFAVINSNYALSANLNPAK
DSVFIEDK
DSVFIEDKESPYANILVVR
20 EGVKIAIPNDPTNESR
ESPYANILVVR
FVELKPAQLPR
IAIPNDPTNESR
IKFVELKPAQLPR
25 IKQFIIEK
QFILEKYNGSVLPAF
QGYKLEIK
SLDDIKEGVK
TPLDIIDNPK
30 TPLDTIIDNPKK
VAAIHIEPMAVYSK
VAAIHIEPMAVYSKK
VGHENDPK
VGHENDPKIK
35 YKSLDDIK
YNGSVLPAF

Sequence: AnrP191193

40 AKDLSVIEIGAAGK
AVFVIKEGK
DLSVIEIGAAGK
EFGEKVGVLINEGALEGLLAR
ELVNEITIEMPDIAK
45 FCSTEGIENLSVASDFVAK
FCSTEGIENLSVASDFVAKERFGEK
GNSVEVGADAPK
KVASYNGAEVIVVSMILPFAMGR
LDAFFGGSSCCGGCGCH
50 LKGNSVEVGADAPK
MSIVNFK
SIVNFKGNPVK
TQIILSVPSLDTPVCATEAR
TQIILSVPSLDTPVCATEAREFNK
55 VASYNGAEVIVVSMILPFAMGR
VAYKELVNEITIEMPDIAK
YGVVLINKEGALEGLLAR

P814 DK00

71

Sequence: AnrP694298

5 AKEILSEFQQR
 CIHCYNNHK
 DASYSDSLSHK
 DASYSDSLSHKLADVYFVSYFLNK
 DEQNGKDASYSDSLSHK
 EAFBNLHFK
 EILSEFQQR
 10 EILSEFQRANDIAK
 LADVYFVSYFLNK
 LADVVFVSYFLNKQR
 LREAFFPNLHFK
 LYPVSLMNGEFSK
 15 LYPVSLMNCEPSKEMNELFTFAQYK
 MRNFFCK
 NFSNLDEFYDIGLK
 QRNFNSNLDEFYDIGLK
 TYGTPAFVVNGK
 20 YQINPSSAINSMQDLEDLVK
 =====
 Sequence: AnrP318705

25 AKSSTELK
 DTKVNLSDLK
 KPIIKDTK
 MMMQKIPETIIK
 NIDSKEF
 SDISEVSELHTHINK
 30 SDISEVSELHTHINKDGK
 SGGYHIMLLK
 SGGYHIMLLKLK
 VNLDLKFNNHK
 =====
 35 Sequence: AnrP493933

40 ALFLSSNDLQLSR
 ALLCFIDNQR
 ALLCFIDNQRGR
 AMSVANKDAILLHCLPAYR
 DAIILHCLPAYR
 DKDVITDTWVSMGEENEK
 DTARVIGAMVDFVMMR
 DVVITDTWVSMGEENEK
 45 DVVITDTWVSMGEENEKER
 EEILSLVNHASELK
 EEILSLVNHASELKK
 EFEGPMIDEK
 EWNKMQNGIAK
 50 FEALKDK
 GEPVKDTAR
 GYEVSEEIFEK
 HADVIFEEAR
 HETLLEFAR
 55 HETLLEFARYSK
 HFLTLRDFSK
 IKEFEGPMIDEK
 ISLGVDKFEALK
 ISPEIWEFAMK

P814 DK00

72

ISPEIWEFAMKQALISGAK

KHFLTLR

LLQDKTLAMIFEK

LYVVKALLCFLDNQR

5 MAFELAITELGK

MKHFLTLR

NRLYVVK

NYKISPEIWEFAMK

QALISGAKISLGYDK

10 TLAMIFEK

TLAMIFEKNSTR

TRMAFELATTETGGK

VIGAMVDFVMMR

VIGAMVDFVMMRVNK

15 VNKHETLLEFAR

Sequence: AnrP979073

ATIKPSNAPMGEGNNDIITNNITK

20 DMI GTKGEFK

DNKFEAK

GEFKNVEYK

GQLDLHTPK

GVISAKITMDK

25 ISPEGYK

KSTIVPLTYTIK

NIKDLASYLK

NVEYKF SK

STIVPLTYTIK

30 STIVPLTYTIKD NK

TKDMIGTK

VFFPALLGDTDIK

VVFQDVIAGENK

VVFQDVIAGENKGVISAK

35 Sequence: AnrP257863

EFISVYEK

GDKLESSSGANR

40 IGVVLPLSGATAAYGQSALEGIK

IPLIAPAATGDR

LANSMQSALSNGDK

LANSMQSALSNGDKVSLAIIDTK

LSKEFISVYEK

45 NYQGVSGVISIDQTGNATR

QNYKDIINP

QYKSNGGQILR

SAVIVVDQSTDYSLGLAK

SLNPEFIFLPLYYSEASLFAR

50 SNGGQILR

SVVVKEIK

VAEDNKIPLIAPAATGDR

VCFMDSFQGSSLAK

VIGLIG2MVNTANTLQVMR

55 VNSGDKDFR

VSLAIIDTK

VSLAIIDTKGDK

P814 DK00

73

Sequence: AnrP326257

AFENSFK
 AFENSFKNNNGK
 5 DFQAVGGVISIDESGNAIR
 DFVAAYEK
 EIQNQKQNYK
 FATYVSKDLGLK
 GDKLETSGVNR
 10 IHQTKDFQAVGGVISIDESGNAIR
 IPLIAPVASGDK
 KTPITAPVASGDK
 KLVINSGDK
 LETSNGVNR
 15 LSNGDVIKLITIDTK
 LVINSGDK
 LVINSGDKDFR
 NAVIIIDQSNVYSLGLAR
 NNGGKIIK
 20 QNYKTIINP
 SLNPDFVYMPIYHPEAALIAR
 SVVIKEIQNOK
 VCFKDQFQGDK
 YASRVCFK
 25 ======
 Sequence: AnrP198268

DNDGFISK
 EIFNLPIK
 30 ELSIIKNEK
 ESYDGIVFYK
 FGGPNGLYLDR
 FGGPNGLYLDRK
 FLTHLNAPK
 35 GAIFLNDIEK
 IFKVELINK
 LELPLMK
 QYDELLK
 SPESIFVDK
 40 TKQYDELLK
 TLYVVVIDVLR
 YQEFDGPK
 YQEFDGPKSPESIFVDK
 45 ======
 Sequence: AnrP515430

ABEVITALK
 AGVNNYIVKPFTPQVLK
 EKLEDVLGTGSGEAAE
 50 IIKNTLTR
 KYEDMPIIMVTTEGGK
 LEDVLGTGSGEAAE
 LLVVDDDSSTMRR
 55 LLVVDDDSSTMRR
 MKLLVVDDDSSTMRR
 YEDMPIIMVTTEGGK
 ======

P814 DK00

74

Sequence: AnrP385049

AIEAHIELK
CAVCHGANADK
5 CAVCHGANADKVYLNK
EYSEGKR
GLTEEDFK
GLTEEDFKATEAHIELK
KCAVCHGANADK
10 LLVVSALACLGVSafaADGATLKK
LNLKGLTEEDPK
LQYMKEYSEGK
NAYGQGAIMK
NAYGQGAIMKLNLK
15 RNAYGQGAIMK
VPALKTLSSAER
VYLNKVPALK

=====

Sequence: AnrP470247

20 DSDDDIKLYSSGVVVQHFSNSQSIIAR
EFPQIYPTTHIDIFGAQLIR
GLVIAPDBQTYNELVR
LEFSVFSALK
25 LEFSVFSALKQDALPLPNVLPK
LYEVPISKPTSVQVPPFYSR
LYSSGVVVQHFSNSQSIIAR
QDALPLPNVLPK
SELVKVDDIYGYIK
30 SNFFDFNSQEIGNYYR
TATLSPKR
VDDIYGYIK
VDDIYGYIKDSDDIK
VGDEVVILNFLYDR
35 YYDALINLPK
YYDALINLPKVQ

=====

Sequence: AnrP679791

40 ANRPSPLDDFFNDPYFK
AYKNQEGALITDVQK
DGENKQASFILK
DGYIVTNHVVDDADTTITVNLPGSDIEYK
DNIGLNOYENFIQTDAISINPGNSGGALVDSR
45 DRLQIPK
DVNGVLVDSVK
DVNGVLVDSVKEK
ENPKGVQSDLIDGLSLR
GFLGVТИLALQGDTK
50 GFLGVТИLALQGDTK
GGGMNGIGFAIPSNNMK
GKNSGFQEGDIIIGVGQSEIK
GSSADEAGLK
GSSADEAGLKR
55 GVQSDLIDGLSLR
GYLVGINSAILSR
IDRGFLGVТИLALQGDTK
ISLSYER
ISLSYERDGENK

P814 DK00

75

KSVVNISTSK
 NGFATLVLK
 NLKDLEQALK
 NQEGALITDVQK
 5 NSGFQEIIDIIIGVGQSEIK
 NYIGTLEIGOK
 QASFILGEK
 SPIDLKNYIGTLEIGQK
 SVVNISTSK
 10 VNPAAGNAVLSYHDSIK
 VNPAAGNAVLSYHDSIKDAK.
 ======
 Sequence: AnrP530915

15 AAVSTAVAAAAAVK
 AAVSTAVAAA AVKDGVAK
 ALAPTVGGINLEDIAAPK
 ANLVAITVSDGSAVLGLGNIGAQASKPVMEGK
 AYFESLK
 20 AYNLSTLEFGR
 AYNLSTLEFGRDYVIPKPFDER
 DNELAYTYTNK
 DFVIFALANPIPEVMPEDVAR
 DRNDLTQPK
 25 DYVIPKPFDER
 GADVFLGLSAPK
 GALDVRASK
 ILDEDEMVL SMAK
 KAYNLSTLEFGR
 30 LEFAVDISK
 LEFAVDISK
 LPVSDAVKK
 MNLKBEALK
 NDLTQPKLEFAVDISK
 35 NFDEKAYFESLK
 NLGVENTILVDSK
 NLKEEALK
 SDYPNQINNVLGFPPTFR
 TLKEVLK
 40 VKNFDEK
 VVVSGAGAAGIASAK
 ======
 Sequence: AnrP108083

45 AQFPNATVSVSNR
 AQFPNATVSVSNRQK
 AVAQKETMVIALGDK
 DSLITPDLIIDLK
 EHLAQIDDELK
 50 EHLAQIDDELKNYQVNYYILTPVHGK
 ETMVIALGDK
 EVFSLYEK
 NKPAIYVFSDPECPYCR
 NYQVNYYILTPVHGK
 55 QENILFTK
 SLGLSATPTIICK
 TGISYAQEYEMK
 TGISYAQEYEMKK
 VGNTGFESVIVSVELNGQK

P814 DK00

76

VSDAELKEVPSLYEK
YYDANIK
YYDANIKNYPK

5 Séquence: AnrP947055

AQIELQTR
ASELLLLK
ASFEALQK
10 ASFEALQKER
DAALADVL SQMDAEDASK
EAEVNATLAK
EIYSOMIK
15 EIYSQMDAALADVL SQMDAEDASK
ERLENLEK
IEELKLENAR
ILNSINDK
ILNSINDKTQGR
IMLSLESR
20 IMLSLESRK
ISGVLSKMDPK
KAQIELQTR
KASELTLLLK
QSLEYRK
25 VKEIYSQMK

Sequence: AnrP407504 ,

AEEFRAFRK
AFRDTINVRPNEELR
AIYKEELFLSPASR
ALFLKNESK
ATLEIKENHIELIK
DALSHLKEK
30 DLMISDLR
DTINVRPNEELR
DTINVRPNEELRLK
EATTIHWHGVPVPPDQDGSPHDOPILAGEER
EELFLSPASR
40 EELFLSPASRVEVLIDAPK
EESNTLFLANINLK
EFKEIJMSEDHMOMHGMMGK
EGEFVLINGQFKPK
EGEFVLINGQFKPKIK
45 ETIMSEDHMOMHGMMGK
ETIMSEDHMOMHGMMGKSENELK
EKDLMISDLR
EKLELPK
ENHIELIK
50 ENHIELIKGK
PEIPQDSAGTYWYHPHPHYTASK
FILVGTDGGGLIEK
FILVGTDGGGLIEKAIYK
I ALASMFLINGK
55 I ALASMFLINGKS YDLK
IDLSSKLGVVEDWIVINK
IEVFEGDK
IEVFEGDKLEILVK
IFKPPLKEPK

P814 DK00

77

IFKPLEEPKEFK
 IKLATNER
 IRIYNATAAR
 IYNATAAR
 5 IYNATAARYINLR
 IYRFEIPQDSAGTYWYHPHPHYTASK
 KDALSHLK
 KTLFYTNGLVPAPK
 LATNERIR
 10 LDENAQIPNNNLNDWLNGR
 LELPKNLK
 LESAYYDR
 LESAYYDRDK
 LGVVEDWIVINK
 15 LLDPKQFPQGEILK
 MMVKEESNTLFLANINLK
 MYHCHILLEHEDLGMGNLEVK
 MYHCHILLEHEDLGMGNLEVKE
 NFLKFNALTLASMGVAYANPMHDHMHSMHK
 20 NHSINHLDLTSFINFAPK
 NHSINHLDLTSFINFAPKONLK
 NIFRATLEIK
 NLKIEFKPLEEPK
 NLKLLDPK
 25 QDFKGCLR
 QFPQGEILK
 QVFMGLAGAFVIK
 QVFMGLAGAFVIKAK
 SENEKIALASMFLINGK
 30 SHMDHPFHNGTQFELISSK
 TLFYTYINGLVPAPK
 TLFYTYINGLVPAPKLEVPEGDK
 VEVLIDAPK
 35 VEVLIDAPKDGNPK
 VQKAEFR
 YLNLRIGQAK
 ======
 Sequence: AnrP818860
 40 AEKEPMK
 ESLELIKNEK
 GKPNLVIVNEGDDSLK
 GKPNLVIVNEGDDSLKNFYSVIATNPK
 GTYTKYEANEK
 45 KGVILTDR
 LLNKPLFVIDAK
 LTFISRGDK
 MATTSTDNTGLLDALKPLYEK
 MGEDCNADVLFVHSPK
 50 NEYSVIATNPK
 NLKESLELIK
 NVNYTEASK
 QSWYQQSGQQMLASIK
 SGTDNKEK
 55 TLNFIADEFK
 TEVVMYNDIIJADK
 WVAVGTGAALK
 ======

P814 DK00

78

Sequence: AnrP355324

5 AEDLLVSAAGPK
 AEDLLVSAAGFKK
 ALMFNLDNEFLK
 ALMFNLDNEFLKD
 ANEHFYLDK
 ANEHFYLDKV
 ARNTSNLEER
 10 DDVLWHDGVKFSDADDVK
 DTLIIAVENEIAR
 FDENMSLKPDLAK
 FDENMSLKPDLAKSWDISK
 FSIEAFK
 15 FSIEAFKNPK
 HIFDPSTASAEKL
 ILEFEIWAMSNDPLR
 INPAYSEDHDAVINLVFSGLTR
 IYKYDPK
 20 KGEYVEFK
 KV DIALQK
 NDENFGILRK
 NKDG NPEK
 25 NLLHDYAFVANHPLER
 NTSNLEER
 QALNYAVDKESIVK
 SVEILNP SHVK
 TLGHGVGFTWNVYEW SK
 30 TPRLI IK
 VDIALQKAR
 VSLAGI LQSEFR
 VSLAGI LQSEFRK
 VVAKPAGSF DYSK
 35 ======
 Sequence: AnrP111949

40 AEDQIVGIATLQHSNIYPK
 AERLEDITK
 EKEAELK
 IIDRIQE FK
 KLSDKPLNK
 LSDKPLNK
 LTSVGTFSNPSLEK
 45 NITTIGQITK
 NLSPQSQISRPVISAEYILK
 NNLLDTNALLK
 QNPDI LILGINAK
 SINLKAER
 50 ======
 Sequence: AnrP294550

55 ELNGMETA AVYLQPIEMEPR
 FKYTGT PK
 GGFVGVGN YELTFYI SNPEK
 GGFVGVGN YELTFYI SNPEKQGPGR
 GIDLAA SLADITHLEADIHALK
 GTLMMPMVADDGPHYGANIAMEK
 GTLMMPMVADDGPHYGANIAMEKDK

P814 DK00

79

HVDEETGVGK
HVDEETGVGKWFEPFK
KGPGVGNYELTFYTSNPEK

5 QGFGRREVDEETGVGK
RGTLMPMVADDGPHYGANTAMEK
WFEPFK
WFEPFKVDYK

10 Sequence: AnrP407676

ASMLNYEGMPAFALSENLAVLK
DNMDLNISTEVFAK
ELQNLISAGNDFSILTER
15 FEDPLAGYER
FNLFDPSKPKPK
FQFFIR
GSTLYFQVLRDNMOLNISTEVFAK
IGLLGTPCCCEMMGIALNNSSFIGNR

20 IYVNNVR
LNEKILFADR
NDWVGIWDPNKPYIGHIK
NPQFLINDQVISVDGLPANDLR
NPQFLINDQVISVDGLPANDLR
25 TDFSLIPTPMGDEEK
TDFSLIPTPMGDEEKLTR
YDPFLNLYLVR
YLAQNIIDEK
YLAQNIIDERDQLDFNSK
30 YLKHEMK

P814 DK00

80

Claims

1. A vaccine comprising:
 - a polypeptide comprising a sequence having at least 95% sequence identity to any of the sequences selected from the group of surface-located *Campylobacter jejuni* polypeptides of SEQ ID NO:1-51, or comprising an antigenic fragment of any of said sequences,
 - a polynucleotide comprising a sequence encoding said polypeptide,
 - an expression vector comprising a sequence encoding said polypeptide,
 - or
 - a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector.
2. The vaccine of claim 1, wherein the fragment comprises 6 or more consecutive amino acids of said sequence.
3. The vaccine of claim 1 or 2, wherein the fragment comprises less than 99%, such as less than 75%, e.g. less than 50%, such as less than 25%, e.g. less than 20%, such as less than 15%, or e.g. less than 10% of the full-length of said sequence.
4. The vaccine of any of claims 1-3, wherein the fragment comprises less than 70 consecutive amino acid residues, e.g. less than 50, such as less than 40, e.g. less than 30, such as less than consecutive 20 residues of said sequence.
5. The vaccine of any of claims 1-4, wherein the fragment comprises 6 or more, such as 7 or more, e.g. 8 or more, such as 9 or more, e.g. 10 or more consecutive amino acids of said sequence.
- 30 6. The vaccine of any of claims 1-5, wherein the fragment comprises one or more residues of any of the fragments of SEQ ID NO:52-119, e.g. two or more consecutive, such as three or more consecutive, e.g. four or more consecutive, such as 5 or more consecutive residues, e.g. 6 or more consecutive residues of any of the fragments of SEQ ID NO:52-119.

P814 DK00

81

7. The vaccine of any of the preceding claims, wherein the polypeptide has at least 96%, e.g. at least 97%, such as at least 98%, e.g. at least 99%, such as 100% sequence identity to any of said sequences.
- 5 8. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:1, or an antigenic fragment thereof.
9. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:2, or an antigenic fragment thereof.
- 10 10. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:3, or an antigenic fragment thereof.
11. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:4, or an antigenic fragment thereof.
- 15 12. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:5, or an antigenic fragment thereof.
- 20 13. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:6, or an antigenic fragment thereof.
14. The vaccine of any of claims 1-7; wherein the polypeptide comprises SEQ ID NO:7, or an antigenic fragment thereof.
- 25 15. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:8, or an antigenic fragment thereof.
- 30 16. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:9, or an antigenic fragment thereof.
17. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:10, or an antigenic fragment thereof.

P814 DK00

82

18. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:11, or an antigenic fragment thereof.
19. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:12, or an antigenic fragment thereof.
5
20. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:13, or an antigenic fragment thereof.
- 10 21. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:14, or an antigenic fragment thereof.
22. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:15, or an antigenic fragment thereof.
15
23. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:16, or an antigenic fragment thereof.
24. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:17, or an antigenic fragment thereof.
20
25. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:18, or an antigenic fragment thereof.
25
26. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:19, or an antigenic fragment thereof.
27. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:20 or an antigenic fragment thereof.
30
28. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:21, or an antigenic fragment thereof.
29. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:22, or an antigenic fragment thereof.
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P814 DK00

83

30. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:23, or an antigenic fragment thereof.
- 5 31. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:24, or an antigenic fragment thereof.
- 10 32. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:25, or an antigenic fragment thereof.
- 15 33. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:26, or an antigenic fragment thereof.
- 20 34. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:27, or an antigenic fragment thereof.
- 25 35. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:28, or an antigenic fragment thereof.
- 30 36. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:29, or an antigenic fragment thereof.
- 35 37. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:30, or an antigenic fragment thereof.
- 40 38. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:31, or an antigenic fragment thereof.
- 45 39. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:32, or an antigenic fragment thereof.
- 50 40. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:33, or an antigenic fragment thereof.

P814 DK00

84

41. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:34, or an antigenic fragment thereof.
42. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:35, or an antigenic fragment thereof.
5 |
43. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:36, or an antigenic fragment thereof.
- 10 44. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:37, or an antigenic fragment thereof.
45. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:38, or an antigenic fragment thereof.
15 |
46. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:39, or an antigenic fragment thereof.
47. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:40, or an antigenic fragment thereof.
20 |
48. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:41, or an antigenic fragment thereof.
- 25 49. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:42, or an antigenic fragment thereof.
50. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:43, or an antigenic fragment thereof.
30 |
51. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:44, or an antigenic fragment thereof.
- 35 52. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:45, or an antigenic fragment thereof.

P814 DK00

85

53. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:46, or an antigenic fragment thereof.
- 5 54. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:47, or an antigenic fragment thereof.
55. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:48, or an antigenic fragment thereof.
10
56. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:49, or an antigenic fragment thereof.
57. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:50, or an antigenic fragment thereof.
15
58. The vaccine of any of claims 1-7, wherein the polypeptide comprises SEQ ID NO:51, or an antigenic fragment thereof.
- 20 59. The vaccine of any of the preceding claims, wherein the vaccine further comprises an immunogenic carrier, such as a carrier protein, wherein the carrier is preferably bound, covalently or non-covalently, to said polypeptide.
60. The vaccine of any of the preceding claims, wherein the recombinant cell is an attenuated or reduced-virulence *Escherichia coli* or *Salmonella* cell.
25
61. The vaccine of any of claims 1-60, wherein the recombinant cell is alive.
62. The vaccine of any of claims 1-60, wherein the recombinant cell is dead.
30
63. The vaccine of any of the preceding claims, further comprising an adjuvant.
64. The vaccine of any of the preceding claims, wherein the vaccine is suitable for systemic administration.
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P814 DK00

86

65. The vaccine of any of the claims 1-63, wherein the vaccine is suitable for intravenous, intramuscular, or subcutaneous administration.

5 66. The vaccine of any of the claims 1-63, wherein the vaccine is suitable for oral administration.

10 67. The vaccine of any of the claims 1-63, wherein the vaccine is suitable for intranasal administration.

15 68. An antibody capable of specifically binding any of the polypeptides of SEQ ID NO:1-36 or a fragment thereof.

20 69. The antibody of claim 68, wherein the antibody furthermore is capable of specifically binding an intact *Campylobacter jejuni* cell.

25 70. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:1, or a fragment thereof.

30 71. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:2, or a fragment thereof.

35 72. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:3, or a fragment thereof.

 73. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:4, or a fragment thereof.

 74. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:5, or a fragment thereof.

 75. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:6, or a fragment thereof.

 76. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:7, or a fragment thereof.

P814 DK00

87

77. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:8, or a fragment thereof.

5 78. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:9, or a fragment thereof.

10 79. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:10, or a fragment thereof.

15 80. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:11, or a fragment thereof.

20 81. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:12, or a fragment thereof.

25 82. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:13, or a fragment thereof.

30 83. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:14, or a fragment thereof.

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 84. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:15, or a fragment thereof.

 |

 85. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:16, or a fragment thereof.

 |

 86. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:17, or a fragment thereof.

 |

 87. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:18, or a fragment thereof.

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P814 DK00

88

88. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:19, or a fragment thereof.
- 5 89. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:20, or a fragment thereof.
90. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:21, or a fragment thereof.
- 10 91. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:22, or a fragment thereof.
92. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:23, or a fragment thereof.
- 15 93. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:24, or a fragment thereof.
94. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:25, or a fragment thereof.
- 20 95. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:26, or a fragment thereof.
- 25 96. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:27, or a fragment thereof.
97. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:28, or a fragment thereof.
- 30 98. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:29, or a fragment thereof.
- 35 99. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:30, or a fragment thereof.

P814 DK00

89

100. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:31, or a fragment thereof.
- 5 101. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:32, or a fragment thereof.
102. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:33, or a fragment thereof.
- 10 103. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:34, or a fragment thereof.
- 15 104. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:35, or a fragment thereof.
105. The antibody of any of claims 68-69, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:36, or a fragment thereof.
- 20 106. An antibody capable of specifically binding any of the polypeptides of SEQ ID NO:37-51 and capable of specifically binding an intact *Campylobacter jejuni* cell.
- 25 107. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:37, or a fragment thereof.
108. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:38, or a fragment thereof.
- 30 109. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:39, or a fragment thereof.
110. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:40, or a fragment thereof.

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PB14 DK00

90

111. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:41, or a fragment thereof.
- 5 112. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:42, or a fragment thereof.
113. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:43, or a fragment thereof.
- 10 114. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:44, or a fragment thereof.
115. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:45, or a fragment thereof.
- 15 116. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:46, or a fragment thereof.
117. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:47, or a fragment thereof.
- 20 118. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:48, or a fragment thereof.
- 25 119. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:50, or a fragment thereof.
120. The antibody of claim 106, wherein the antibody is capable of specifically binding the polypeptide of SEQ ID NO:51, or a fragment thereof.
- 30 121. The antibody of any of claims 68 to 120, wherein the antibody is polyclonal.
122. The antibody of any of claims 68 to 120, wherein the antibody is monoclonal.

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P814 DK00

91

123. The antibody of claim 121 or 122, wherein the antibody is a human or humanised antibody;

5 124. The antibody of claim 123, wherein the antibody is a human antibody.

10 125. The antibody of any of claims 68-124, wherein the antibody is a binding fragment of an antibody.

15 126. The antibody of any of claims 68-125, wherein the antibody has a dissociation constant or Kd less than 5×10^{-6} M, such as less than 10^{-8} M, e.g. less than 5×10^{-7} M, such as less than 10^{-7} M, e.g. less than 5×10^{-6} M, such as less than 10^{-8} M, e.g. less than 5×10^{-9} M, such as less than 10^{-9} M, e.g. less than 5×10^{-10} M, such as less than 10^{-10} M, e.g. less than 5×10^{-11} M, such as less than 10^{-11} M, e.g. less than 5×10^{-12} M, such as less than 10^{-12} M, e.g. less than 5×10^{-13} M, such as less than 10^{-13} M, e.g. less than 5×10^{-14} M, such as less than 10^{-14} M, e.g. less than 5×10^{-15} M, or less than 10^{-15} M.

20 127. A pharmaceutical composition comprising a pharmaceutically-acceptable carrier and

25 - an isolated polypeptide which comprises any of the sequences of SEQ ID NO:1-36, or comprises a fragment or variant of any of said sequences,

- an isolated polynucleotide comprising a sequence encoding said polypeptide,

- an expression vector comprising a sequence encoding said polypeptide,

30 or

- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector.

128. A pharmaceutical composition comprising an antibody as defined in any of claims 68-126 and a pharmaceutically-acceptable carrier.

35 129. A fragment of any of the polypeptides of SEQ ID NO:1-51, wherein the fragment is antigenic.

130. The fragment of claim 129, wherein the fragment is surface-exposed.

P814 DK00

92

131. The fragment of claim 129 or 130, wherein the fragment is capable of inducing antibodies that can specifically bind an intact *Campylobacter jejuni* cell.
- 5 132. The fragment of any of claims 129-131, wherein the fragment comprises one or more residues of any of the fragments of SEQ ID NO:52-119, e.g. two or more consecutive, such as three or more consecutive, e.g. four or more consecutive, such as 5 or more consecutive residues, e.g. 6 or more consecutive residues of any of the fragments of SEQ ID NO:52-119.
- 10 133. An isolated polynucleotide comprising a sequence encoding the antigenic fragment of any of claims 129-132, wherein said polynucleotide does not comprise a sequence encoding the full-length polypeptide of any of SEQ ID NO:1-51.
- 15 134. An expression vector suitable for DNA vaccination comprising a sequence encoding a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, or comprises a fragment or variant of any of said sequences.
- 20 135. An expression vector comprising a polynucleotide sequence encoding a polypeptide which comprises any of the sequences of SEQ ID NO:1-36, or comprises an antigenic fragment or variant of any of said sequences, said polynucleotide sequence being under the control of a promoter that directs expression of the sequence in *Escherichia coli* or *Salmonella*.
- 25 136. A recombinant cell transformed or transfected with a polynucleotide comprising a sequence encoding a polypeptide, said polypeptide comprising any of the sequences of SEQ ID NO:1-36, or comprising an antigenic fragment or variant of any of said sequences.
- 30 137. The recombinant cell of claim 136, wherein the recombinant host cell is an *Escherichia coli* or *Salmonella* cell.
- 35 138. The recombinant cell of claim 136 or 137, wherein recombinant the cell is an attenuated or reduced-virulence cell.

P814 DK00

93

139. A recombinant attenuated or reduced-virulence *Escherichia coli* or *Salmonella* cell transformed or transfected with a polynucleotide comprising a sequence encoding a polypeptide, said polypeptide comprising any of the sequences of SEQ ID NO:37-51, or comprising an antigenic fragment or variant of any of said sequences.

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140. A composition comprising a carrier and any one or more of

- an antibody as defined in any of claims 68-126,
- a fragment as defined in any of claims 129-132,
- a polynucleotide as defined in claim 133,
- an expression vector as defined in claim 134 or 135,
- a recombinant cell as defined in any of claims 136-138,
- an *Escherichia coli* or *Salmonella* cell as defined in claim 139,

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141. Any one of the following

- a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, or comprises a fragment or variant of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector,
- an antibody capable of specifically binding said polypeptide,
or
- a composition as defined in claim 140,
for use as a medicament.

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142. Use of

- a polypeptide which comprises any of the sequences of SEQ ID NO:1-51, or comprises a fragment or variant of any of said sequences,
- a polynucleotide comprising a sequence encoding said polypeptide,
- an expression vector comprising a sequence encoding said polypeptide,
- a recombinant virus or recombinant cell comprising said polynucleotide or said expression vector,
- or

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P814 DK00

94

- a composition as defined in claim 140,
for the preparation of a medicament for the immunisation of an animal or human
being against *Campylobacter jejuni* infections.

5 143. The use of claim 142, wherein the immunisation induces a protective
immune response.

144. The use of claim 142 or 143, wherein the medicament is a medicament
suitable for parenteral, intravenous, intramuscular, subcutaneous, oral or
10 intranasal administration.

145. Use of an antibody as defined in any of claims 68-126, for the manufacture
of a medicament for the treatment or prevention of *Campylobacter jejuni*
infections in an animal or human being.

15 146. The use of any of claims 142-145, wherein the animal is a chicken, duck,
turkey, cow or pig.

20 147. The use of any of claims 142-145, wherein the human being is in an at-risk
population, such as the population of immunocompromised patients, the
population of children up to 4 years old, the population of persons in
industrialised nations or the population of naive or semi-immune travellers to the
developing world.

25 148. A method for raising specific antibodies to a polypeptide of any of SEQ ID
NO:1-36 in an (non-human) animal comprising the steps of

a. providing

- a polypeptide comprising any of the sequences of SEQ ID NO:1-36, or
comprising a fragment or variant thereof,

30 - a polynucleotide comprising a sequence encoding said polypeptide,

- an expression vector comprising a sequence encoding said polypeptide,
or

- a recombinant cell as defined in any of claims 136-138,

35 b. introducing a composition comprising said polypeptide, polynucleotide, vector or
recombinant cell into said animal,

P814 DK00

95

- c. raising antibodies in said animal, and
- d. isolating and optionally purifying the antibodies.

149. A method for raising specific antibodies to a polypeptide of any of SEQ ID

5 NO:37-51 in an (non-human) animal wherein the antibodies are capable of specifically binding an intact *Campylobacter jejuni* cell, the method comprising the steps of

- a. providing
 - a polypeptide comprising any of the sequences of SEQ ID NO:37-51, or comprising a fragment or variant thereof,
 - a polynucleotide comprising a sequence encoding said polypeptide,
 - an expression vector comprising a sequence encoding said polypeptide, or
 - a recombinant *Escherichia coli* or *Salmonella* cell as defined in claim 139,
- b. introducing a composition comprising said polypeptide, polynucleotide, vector or recombinant cell into said animal,
- c. raising antibodies in said animal,
- d. isolating and optionally purifying the antibodies, and
- e. selecting antibodies capable of specifically binding an intact *Campylobacter jejuni* cell.

150. The method of claim 148 or 149, wherein the raising of antibodies is done in a transgenic animal which can produce human antibodies.

25 151. A method for detecting *Campylobacter jejuni* comprising the steps of

- a. providing a biological sample,
- b. contacting said sample with an indicator moiety capable of specifically binding any of the polypeptides of SEQ ID NO:1-36, and
- c. determining whether a signal has been generated by the indicator moiety.

30 152. The method of claim 151, wherein the indicator moiety furthermore is capable of specifically binding intact *Campylobacter jejuni* cells.

35 153. A method for detecting *Campylobacter jejuni* comprising the steps of

- a. providing a biological sample,

P814 DK00

96

- b. contacting said sample with an indicator moiety capable of specifically binding any of the polypeptides of SEQ ID NO:37-51, wherein the indicator moiety furthermore is capable of specifically binding intact *Campylobacter jejuni* cells, and
- 5 c. determining whether a signal has been generated by the indicator moiety.

154. The method of any of claims 151-153, wherein said indicator moiety does not pass through the outer membrane of a *Campylobacter jejuni* cell.
- 10 155. The method of any of claims 151-154, wherein said indicator moiety is or comprises an antibody, such as an antibody as defined in any of claims 68-126.
- 15 156. A method for identifying a binding partner of any of the polypeptides of SEQ ID NO:1-36 or a fragment thereof, comprising the steps of
 - a. providing any of the polypeptides of SEQ ID NO:1-36 or a fragment thereof,
 - b. contacting said polypeptide or fragment with a putative binding partner, and
 - c. determining whether said putative binding partner is capable of binding to said polypeptide or fragment.
- 20 157. The method of claim 156, wherein the putative binding partner is a host-derived molecule.
158. The method of any of claims 156-157, wherein said method is repeated for a plurality of putative binding partners.
- 25 159. A method for identifying a compound with antibacterial activity against *Campylobacter jejuni* comprising the steps of
 - a. providing a sensitised cell which has a reduced level of any of the polypeptides of SEQ ID NO:1-36, and
 - b. determining the sensitivity of said cell to a putative antibacterial compound, for instance by a growth assay.
- 30 160. The method of claim 159, wherein said method is repeated for a plurality of putative antibacterial compounds.

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P814 DK00

97

161. The method of any of claim 159 or 160, wherein the putative antibacterial compound does not pass through the outer membrane of a *Campylobacter jejuni* cell.

5 162. A method for identifying a compound with antibacterial activity against *Campylobacter jejuni* comprising the steps of

a. providing a sensitised cell which has a reduced level of any of the polypeptides of SEQ ID NO:37-51, and

10 b. determining the sensitivity of said cell to a putative antibacterial compound, for instance by a growth assay, wherein the putative antibacterial compound is not capable of passing through the outer-membrane of a *Campylobacter jejuni* cell.

163. The method of claim 162, wherein said method is repeated for a plurality of putative antibacterial compounds.

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164. A method for finding an inhibitor of any of the polypeptides of SEQ ID NO:1-36 comprising the steps of

a. providing two cells which differ in the level of any of the polypeptides of SEQ ID NO:1-36,

20 b. determining the sensitivity of said cells to a putative inhibitor, for instance by a growth assay, and

c. determining whether said two cells are differently affected by the presence of said putative inhibitor.

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165. The method of claim 164, wherein the two cells differ in the copy number of said polypeptide.

166. The method of claim 164, wherein the two cells differ in the activity of said polypeptide.

30

167. The method of any of claims 164-166, wherein said method is repeated for a plurality of putative Inhibitors.

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168. The method of any of claims 164-167, wherein the putative binding partner does not pass through the outer membrane of a *Campylobacter jejuni* cell.

P814 DK00

98

169. A method for finding an inhibitor of any of the polypeptides of SEQ ID NO:37-51 comprising the steps of

5 a. providing two cells which differ in the level of any of the polypeptides of SEQ ID NO:37-51,

 b. determining the sensitivity of said cells to a putative inhibitor, for instance by a growth assay, wherein the putative inhibitor is not capable of passing through the outer membrane of a *Campylobacter jejuni* cell, and

10 c. determining whether said two cells are differently affected by the presence of said putative inhibitor.

170. The method of claim 169, wherein the two cells differ in the copy number of said polypeptide.

15 171. The method of claim 169, wherein the two cells differ in the activity of said polypeptide.

 172. The method of any of claims 169-171, wherein said method is repeated for a plurality of putative inhibitors.

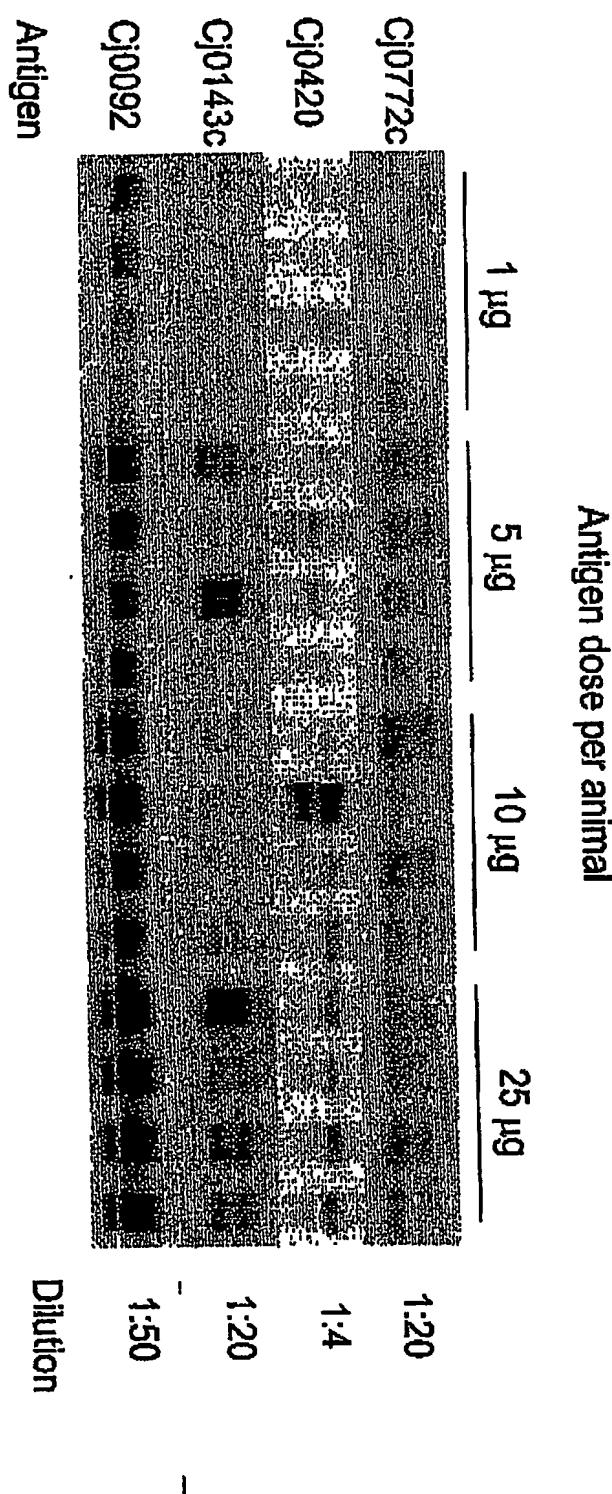
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Patent- og
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21 NOV. 2003

Modtaget

Figure 1



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Figure 2

21 NOV. 2003

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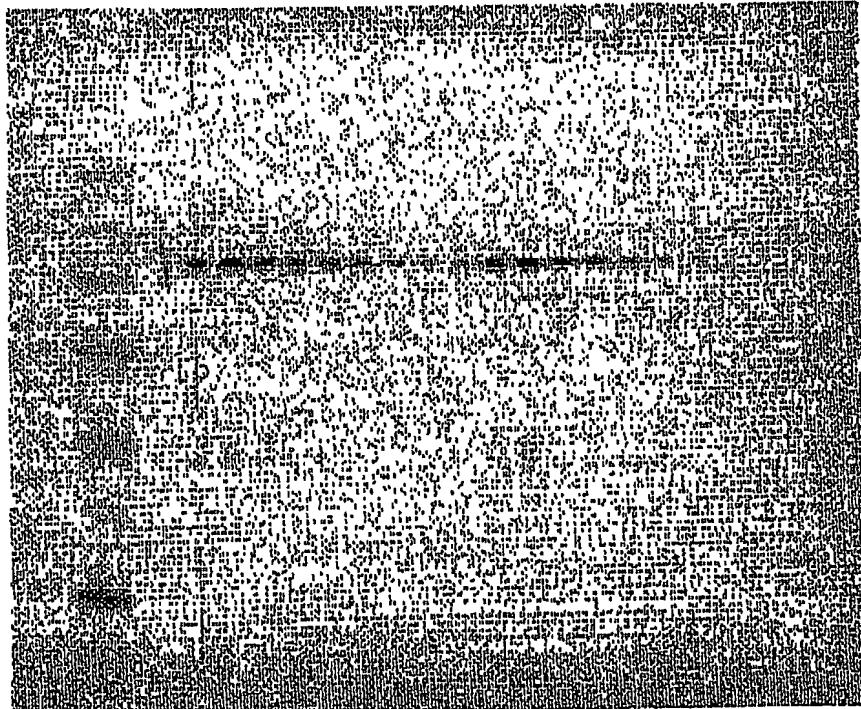
Titration of Antibody against Cj0092 (SEQ ID NO:1).

100ng of purified Cj0092 antigen was loaded on the gel, blotted and probed with different dilutions of mouse anti Cj0092 Antibody.

Dilutions are from left to right (for two individual animals): 1:50, 1:50, 1:100, 1:200, 1:400, 1:800, 1:1600, 1:3200, 1:6400

Lane 1: Marker proteins MW in kD: 97, 64, 51, 39, 28, 19, 14,

The antigen can be seen in all dilutions of the antibodies.



P814DK00

Patent- og
Varemærkestyrelsen

21 NOV. 2003

Sequence listing

Modtaget

SEQ ID NO:1

ACE 83 Cj 0092

>AnrP630851 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKKILFIGSIVMASLLYAQGSQPVEITQQDINTQNEMSDASTKDITPKSIEDFFEEFADNFGIEYGITKD
 GKTFTGKSTVAVNDTDPQFAQALQNAYQKAMLYQSEFIRDAFGRIATSKIQNYEADNSTNAKEFDELP
 KGDKVDQIILNKLTLQLAGAQLDKALKDLGIDTNSLSEDRKKTLLKQEFLNKTMTNAIGSMSGLVPVQTIVT
 ORRGEYDVGVVAVVISNKTROLAKDMALARQSAIKGKGKAISEYLPKDTKGFLNEYGIRLVYDENGAII
 SYGNWGYVADPSNAKKTNILEDRAKETALIMADAIIIEFINTNLSLKDERTTGDTYEEIIKQSINVNDSS
 TQEQTQNITNIIDKVNSKIKASASGKIRGIRTLKKWSYTSENGIEHVGAVRFYSYENLANTNEALNSKEN
 ATKNEAKKSSSIQRSSNVVNSMDDF

SEQ ID NO:2

ACE 5 Cj 0005

>AnrP544820 (NC_002163) putative molybdenum containing oxidoreductase
 [Campylobact
 MKQNDOKENRRDFLKNIGLGLFGISVLSNFSFENFLGSKALAKELPDFKIEGKKDLIYHGEKPLTAETEI
 YALDSDFTPENFFVRNNGLPPSLSTIKERLHKGWITLEIDGESIINKGSYTIEDLKKKFVYTYALTVEC
 GGNGRSEVIPSTKGTQWGYGAVACGRWTGVRLKDILKDCGIKNDAVYIGYYGIDTKLNGEETSPISRGP
 ISKALQDETLIAWAYEGKDIPLVNGYPLRLVCGGYPASTSGKWLKYKISVRNKLIHDGEKMEGGSYKVPVNPV
 KPGDFNYKGEMKIIIESMPIRSVITNIKNGSEIKANKKFEVRGKAWAGELEVSEVYVSNDYGVWTWTAKVE
 KPLNRLAWQKWSAQISIPTKGYYEIWARAIDS5QGNSQPMVIAQWNPGGYINNACHRVNVYGV

SEQ ID NO:3

ACE 29 Cj 0029

>AnrP372217 (NC_002163) cytoplasmic L-asparaginase [Campylobacter jejuni]
 MKKAKSRIAILGTGGTIAGFIDSTIATTGAAAGAIDIDVLIKAVPQIARDLADISWEQIANIDSSNMCDEI
 WLRLAKKIAKLFAEGIDGVVITHGTDTMEETAYFLNLTKSDKPVVLUVGAMRPSTAISADGPKNLYNAVA
 LVVNKEAKNKGVVMVAINDKILSARGVVKTHSILNVDASFSPDFGDLGYTVDGKVFVYNNVIKAHTKNAPFD
 VSKLTSLPKVDILYSYSNDGSGVAAKALFEEGTKGIVVAGSGAGSIHKNQKDVLKELLKKGLKVVVSSRV
 VAGCVAVSDSDEKLGFISAEDLNPQKARVLLMLALTKTSDPKKIQHEYFLKV

SEQ ID NO:4

ACE 37 Cj 0037

>AnrP501075 (NC_002163) putative cytochrome c [Campylobacter jejuni]
 MKKHILLGLCLSLSLAKSVSDYKVGEELSDFKESVYFKELSKREVQEWPNKQLSINDVEKGKQGDLIR
 YGIELLSKTESTLGLPYSKLKKTSNEVNCISCHMDNDGNGLPGTKVYIPFLNILNNYPRLDIETMKIIISV
 EDRIRGMGGTDSHRFPDNSKEMKAIILAYFKWLKEAYGIKDGVKLEGDFFAKMNFPNRPADDVRGKKLFEE
 NCVACHGERGLGVKNDNYEQGSGHLYPSLLIYPDGHHMAMIPFLARFLKSAMPFGASADNPILSDEDALD
 IAAVNTGFRMRMIFTTENRAGIDTAYSKPSLKPKEYFASPQONLDPKEYIKVYGPWKNPHEFPGE

SEQ ID NO:5

ACE 84 Cj 0093

>AnrP666574 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKIIKILFLGLFLSLSLNAKVTTTSTKSSTGEGTGLTREDAINNAITEAIGKMSGVSINSLKKSNNTSVS
 TDNSGSNTQDNYSEQISKATKGRADTYEINSVEQDANGKYTANVTIPKTTTCKYQAPGLSADNRRSITV
 FDSTPDAAKRGIGCSALQQKIIISDLLOSERKFNVLDRDSSGYYEMEKALIKSGDAASDEVYKLKNMLATTYI
 LLFSISGLEGKQKTSNLTGKSCTEIEVIVDVRVLLPATRQIKPSNTLSMKVNLKDNLSSANETALKQIAN
 RIAGDILNAIYPLKVASVENNEVIFSQSLNQGDVYECFALGKVIKDTYTAKENTGRVESKTGSIEITRTSP
 KFSYAKITEGSVKVGDIICRPLSNTGSGNGYTIGRDANYQTQEGGGVNLGF

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SEQ ID NO:6

ACE 98 Cj0107

>AnrP732169 (NC_002163) ATP synthase F1 sector beta subunit [Campylobacter jejuni]
 MQGFISQVLGPVVVDVFNDYLPQINEAIVVNFESSEGKHHKLVLSEVAHLGDNVRVTIAMDMDGLVRGLK
 AEALGAPISVPVGKVLGRIFNVTGDLIDEGEELISFDKKWAIHRDPAPAFEDQSTKSEIFETGIKVVDLLA
 PYAKGGKVGLFGGAGGVGKTVIIMELIHNVAFKHSGYSVFAGVGERTREGNDLYNEMKESNVLDKVALCYG
 QMNEPPGARNRIALTGLTMABYFRDEMGLDVLMPIDNIFRFSQSGSEMSALLGRIPSAGVYQPTLASEMG
 KFQERITSTKKGTSITSVQAVYVPADDLTDPAATVFAHLDATTVLNRAIAEKIYPAVDPLDSTSRLDP
 NIIIGEEHYKVARGVQSVLQKYKDLQDIIAILGMDELSEEDKLVVERARKIEKFLSQPFVVAEVFTGSPGK
 YISLEDTIAGFKGILEGKYDHLPENAFYMGVNIDEAIAKADKLKG

SEQ ID NO:7

ACE 103 Cj0112

>AnrP511634 (NC_002163) periplasmic protein [Campylobacter jejuni]
 MKKIVAAIFLVLFLGSLWAEDPVVIDVVNSGVLPKIIVKDMSNLSDENLKKSFYNIIVNDLKVSSENFEVAN
 ATETSNYIPEBYTLNKNGNTLSLNVKIKAGGSRKSEQTYTNGLEQYPFLAHKSVKASVNAALGLAPVDWMD
 HKILIANRSSSKKSQIIMADYTLTYQKIVIDGGLNLFPKWNKEQTLFYTTAYDHDKPTLYRYDLNTNKA
 SKILSSGGMVVASDVNVDGSKLLVITMAPKDQPDVYLYDINTKNLTQLTNYSGIDVNGNFIGSDDSKVVFV
 SDRLGYENTFMQDLSNSAECQVVFHGRNNSAVSTYKDPLVYSSREPNOAGVFNIIYILMSINSDYIRQLTAN
 GKNLFPRFSSDGGSIVFIKYLGAQSALGVIRVNANKTFYFFLRVGKIQSIDW

SEQ ID NO:8

ACE 134 Cj0143

>AnrP57234 (NC_002163) periplasmic solute binding protein for ABC transport system [Campylobacter jejuni]
 MKKIJILFILSLGIFYTFTQAXNLEQEQQNTSSNLVSVSIAPOAFFVKKIAANTLDVNVLPPNSNEHNPEF
 KPSTMKKLEKSDIYFTIIGLEFEKVFDTDKFKQNFPKLQVINMQKNIALIQTHDTHENSHEHHHEHGHFDP
 HTWLDPILVQTMALNITYDTLJQKYPQNENLYKENLDKFLAELDSLNLQIASKLEKLKNREFVVYHPSWTY
 FAKRYNLTQIPVEILGKEPKSKDLQKLITLMKDKNLKVIJVQNGFPENAAKTLAKECDAKIYKIDHLSYD
 WENELLKTADAFSEHNL

SEQ ID NO:9

ACE 159 Cj0169

>AnrP829849 (NC_002163) superoxide dismutase (Fe) [Campylobacter jejuni]
 MFELRKLPYDTNAFGDFLSAETFSYHHCKHHNTYVTNLNNLIKDETAGKDLVSIIKTSNGGVFNNAAQV
 YNHDFYFDCIKPSTGCGCGGSCQSIDANLQAALKEFGSLLENFKAEFIKGATGVFGSGWFWLVYNTKQNQK
 LEFVGTSNAATPITEDKVPLLVVVDVWEAYYDHRNARPAYLEKFYAHINWEFVAKAYEWALKEGMGSVS
 FYANELHPVK

SEQ ID NO:10

ACE 183 Cj0193c

>AnrP139712 (NC_002163) trigger factor (peptidyl-prolyl cis /trans isomerase, chaperone) [Campylobacter jejuni]
 MEVKAKQLDSVNATASVVKIPSGMIKSEVENLAKKASKSVKMDGFRPGKVPVSAVLKRYERELTQDAEQNL
 FKSAVNSALQELKKENKELVGEPYFEKVFDRKDGEIIIAELLILSFKPEIKLEGYBKLIPEYQTFKVSKKIED
 EKKDELLKRATPEAJKTKRALKEGDFAKFDFEGFVDDKAPEGGKAENYVLEIGSKQFIPGFEDGMVGGMK
 IGEEEKDIKVTFPKKEYGA AHLAGKDAVFVKVHLHEIQLKIPELDDEMLKKLLPGEEKASVEVLDEKLKEOI
 KNEKLFKLVNDDELKGKFADALIEKYNFDLPLKGIVQEQTDMQMRAAFNTFSEKEIISELKASKEKYQEKRDS
 FKEEEAQKSVKLTFI IDELA LKIEVNDQELIQAIYFEAYRYGMNPKEHLENKKQGALPAVMALIEK
 LFNDIFIPKTEKSEKVS KKEKEDK

P814DK00

SEQ ID NO:11

ACE 259 Cj0285c

>AnrP467527 (NC_002163) chemotaxis protein [Campylobacter jejuni]
 MF DENIVKTGSNEMELVDPRIFKQGHDKVYEGIYGVNVSKVREIIKIPSLTELPGVPDYIEGIFDRLRGVV
 IPVVNLAKWMQITEPESTMLKPRVIITFSNLLIGFIVIAEKRIRRINWKDIEPATFSTGSGALDKGKIT
 GVTRIENDEVLLLILDLESVVEDLGIYAPKTDIDFGKIEKPTGTALILDDSMTARKRVKEMMQMGFOVVE
 AKDGVEGINKLELSQTGYGESLNDLKIIVSDVEMPQMDFHFAARIKEDPREFDIPIVFNSSLNEFMN
 EKGVQEAGGEGLVKFNASDFNHEIAKVIKKHQSQEQG

SEQ ID NO:12

ACE 332 Cj0358

>AnrP681041 (NC_002163) putative cytochrome C551 peroxidase [Campylobacter jejuni]
 MKVKSLLIASLVAFSSLNAASLIDEAKNSGLVALPKDQKGVDIELKONGVKASEFTLEKAELGKKLYFEP
 RLSKSGIISCNCTCHNVGLGGTDGISTAIGHKWTANPHHLNSPTVYNANLNNTQFWDGRAGTLADQAKGPI
 QADPEMATPAKLAVERKISSLPEVSEFKKIYGKSGVNFDNIADAIAFERTLITPSRFDKFLEGDEKALT
 KEEQKGLKLFIIDKGCVACHNGVNLLGGNMQAFEVAGKYKFANLGDFKGDANGMVKPTLRNVAETAPYHIN
 GAIWNLKDAIKEMGSVQLGIKISDKBAKSIEFLKSLTGTPAIVYPQLPISTEKTPKPEL

SEQ ID NO:13

ACE 419 Cj0448c

>AnrP569688 (NC_002163) putative MCP-type signal transduction protein [Campylobacter]
 MFGSKINHSDLQKLEENKNLTHKIEKFQSENLELKNTSLEQAALESKLKDLLNVLLTGVLKNITII
 QGDMLENVNKAEVVISSYSKTSLAEMDELNHANSINASLGNNTESANKTRDVAGTILHRSVDBRITNVVINLI
 KIVSDQTNLALNAIAEAAARAGEHGRGFAVVADEVRKLAERTQKATTEVEMNINLLKQNANEMYTQSEQV
 EKISIDSNAHIMSFSKCFTHLVNEAHSTNSNAVGIASEAFVSLAKLDHIAFKLNGYKEIFSKSGKQLADH
 TSCRLLGKWLASTGKSERFGQNKSFILKINEPHEKVHENMNNAITIANTEDISKDITQHSIINKCEVAENASL
 DLFNVFKEMLDSDH

SEQ ID NO:14

ACE 420 Cj0449c

>AnrP852550 (NC_002163) hypothetical protein Cj0449c [Campylobacter jejuni]
 MLHEYRELMSHELKGKDAHFDKLFDKHNELDDMIKDAEEGRTSLSSMEISTLKKEKLVKDELSQYLANYK
 K

SEQ ID NO:15

ACE 481 Cj0511

>AnrP255677 (NC_002163) putative secreted protease [Campylobacter jejuni]
 MMELILKTKRFFAGLAGFATTFLCLFLTSHLQAKVDQKEEQVQKRLAEALDKLTKTLAIVEQYYVDDQNI
 SDLVDXSLSGLLSNLDHSSFLNEKDFNDMKIQTNTGEFGGLGITVGMDGALTVVSPPIBGT PADKAGIKS
 GDIILKINDHEATLGGINLNDAVDKMRGKPKTQITLTIFRKGATCPFDVLTREILIKIESVYAKMIENENIL
 YLRVTNFDRKNNVVVDVASKELKKYPNVKGVILDRLRNPGGLLNQAIGLVLNFVDKGVIVSQKGRIASENQEY
 KADPKNKISMASLVLVNVGGSASASEIVSGALQDLKRGVIVGENTFGKGSVQQITIPINKTEALRLTIARY
 YLPSGRTIQAVGVKPDIIEVFPGKVNTQEDGFSIKESDLKQHLESELEKIDKNKKEDKQENKDNKNLISQK
 QINDDAQLKSAIDTIKILNIKQQQ

SEQ ID NO:16

ACE 528 Cj0559

>AnrP252410 (NC_002163) oxidoreductase [Campylobacter jejuni]
 MKKIDLIVVGAGPTGIGCAVEAKLKNKEVLILEKSNNIQOTLMQFYKDGKRVDKAYRGCEGTNHGHVPFE
 DGTKESTIETFQNALKHEHIEVEFGSEVESVKNENGVFLVSTAKGVYECCKNIIIVAIGRMGKPNKPDYKLP
 MTLTKIINEMANNSVLLGNEKILVVGCGNSAAEYAVDLANSNQVSLCYRKKEFTRLNDINLKDIHEAGNSGK
 VELKLGLIDINEVEDDNGKAKVNFTDGTEDIYIYAIGGSTPLDFLQKCGINVDDKGVPMLDENKQSNV
 KG1PVAGDIATKNGASIVTGLNDAVKILSVL

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SEQ ID NO:17

ACE 582 Cj0613

>AnrP916533 (NC_002163) possible periplasmic phosphate binding protein [Campylobacter]
 MKKILSLSVTSLALCGALNAVDLKIAGSSTVYPPTSFVAEEVASIKNTKTPIVESLGTGGGFKVFCCEGTT
 DISNASRPMKLSEFETCKKAGVTIDIVGMMIGYDGIVLAQNKTNAPLNITKKELFLALAKEIPQNGKLIPI
 PYTNWNQINKNLPNRKIISVYGPSSSGTRDTEELVMSDVKKIPEYKGEYKTIRQDGAYIPSGENDNLI
 VSKLTDKDAFGIFGYSFLVSNSDKINAANIDGVTPEESIADEKYELARSLPIYINAKKNPKEAPDFAK
 IYMSDDLAKSGGELEKIGLVPLSDDKLKASQKHVEDRKILDELVKAGKVP

SEQ ID NO:18

ACE 605 Cj0636

>AnrP136795 (NC_002163) NOL1\NOF2\sun family protein [Campylobacter jejuni]
 MQNLLSSFAQEKNVCVFANTLKTSTEELEKEFLKQNLKEKKINVYCYLFDAKDKAILSSMKAFNEAHFYI
 QNYSSYLCALNLEVKGAGSVLDMCAAPGGKSINLANFMQNTGYLACNEMSDRFFTILQKNLKNYGVNAKV
 FMKDQKNIGNLCPPLFDKILLDAPCSTFAKIGFDLEKSYKEIKNIAKTQKLLLHSALKKIGGELVYST
 CTFTKEENEVEENALKSFKLELLLDIDLENVEAKAGQSEEFABISKRRILPSLDYDGFTIAKLRKLC

SEQ ID NO:19

ACE 667 Cj0706

>AnrP327756 (NC_002163) hypothetical protein Cj0706 [Campylobacter jejuni]
 MNKYLEQLVLLSKIDQEIDSYEPKIDSINKTLKDAELKIEKINADLEKIDEIKDIENOKIQONNAHISEF
 SAKIKDLSKSKSGVVVKTEKEANALKISEDIAKEQQLDAANDBIVRLDKILENKETYKKEEKKIKQEQNIN
 EIRVSIKSEMEVLEKDRMSVYDKTKLVSEMNQKVLSFYEKIRKWAKNTAVVPVKQACYGCFMKIYDKT
 YLSVVVKGBEHTVTCPHGRILYKEQEEQN

SEQ ID NO:20

ACE 676 Cj0715

>AnrP684299 (NC_002163) transthyretin-like periplasmic protein [Campylobacter jeju]
 MFSIKKTLILASVPMFLSATBVQLSTHVLDITSQQPAPKVKVELYKLEANQQWKKVSEEFTEENGRID
 LLPYEKAENRAFGIYKLKFFTQDYYTSHKINTFPFVEVSFELSKDQKHYHVPITLSPFGYSTYRGs

SEQ ID NO:21

ACE 731 Cj0779

>AnrP191193 (NC_002163) probable thiol peroxidase [Campylobacter jejuni]
 MSIVNFKGNPVKLGNSVSEVGADAPKVNLKAKDLSVIEIGAAGKTQIILSVPSIDTPVCATEAREPNNKCV
 MSYNGAEVIVVSMDLPFAMGRFCSTEGIENLSVASDPVAKEFGEKYGVLINEGALEGLLARAADVVIKEGK
 VAYKELVNEITEMPDIAKLDAFFGGSSCCGGCGCH

SEQ ID NO:22

ACE 853 Cj0909

>AnrP318705 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKKILLLGALFAVNWLAVNDIEVKNAFKQTTPHAQNSAIFLTIFNNTNKDIALISAKSDISEVSELHTH
 IHKDGKMMMQKIPETIIKHSSTELKSGGYHIMLLKLKKPIIKDTKVNLSDLKFNNHRTIELKNIDSKEF

SEQ ID NO:23

ACE 937 Cj0994c

>AnrP493933 (NC_002163) ornithine carbamoyltransferase [Campylobacter jejuni]
 MKHFLTLRDFSKEEILSLVNHASLKKPEPKLLQDKTLAMIFEKNSTRTRMAFELAITTELGGKALFLSSN
 DLQLSRGEPVKQDTARVIGAMVDFVMMRVNKHETLLEFARYSKAPVINALSELYHPTQVLGDLPTIKEWNK
 MONGIAKVAFIGDSNNMCNSWLITAAILGFEISIAMPKNYKISPEIWEFAMKQALISGAKISLGYDKFEA
 LKDKDVVITDTWVSMGEENEKERKIKEFEGFMIDEKAMSVANKDAILLHCLPAYRGYEVSEEIFEKHADV
 IFEEARNRLLYVVKALLCPFLDNQRGRE

P814DK00

SEQ ID NO:24

ACE 941 Cj0998c

>AnrP979073 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKKILVSVLSSCLLASALSAVSKEDSLKISFEGYKTKDMIGTKGEFKNVEYKFSKNIKDLASYLKGAKA
 TIKPSNAFMGEGNDIITNNITKVFFPALLGQTDIWKVFQDVIAGENKGVISAKITMDIKSTIVPLTYTIK
 DNKFREAKGQLDLHTFKNGSKALKALSDVAAGHGGISWFLVDISFNADLAE

SEQ ID NO:25

ACE 961 Cj1018c

>AnrP257863 (NC_002163) branched-chain amino-acid ABC transport system periplasmic binding protein [Campylobacter jejuni]
 MKKSLILASILSLSAEEVKIGVVPLSGATAAYGQSALLEGIKLANSMQSALSNGDKVSLAIIDTKGDK
 LELESSGAMRVLVSQDKVIOEMVTANTLQVMRVAEDDNKIFPLIAPATGDRLLDKLYGGRVCFCMDSFGQ
 SSLAKYVFSKLNYKSAVIVVDQSTDYSLGLAKAFEKQYKSNGGQILRLRVNSGDKDFRAIVAQVKSLNP
 EFLIFLPLYYSEASLFLARQSKLAGLNIPMGSADGVADQTFISLAGDASEGYIFTDSFDANNPTTKLSKEFI
 SVYEKAKGTKEVPNFSAMGADAYFVMLNAMNACVENLTSKCVNEKIHQTKNYQGVSGVISIDQTGNATRS
 VVVKEIKNQKQNYKDIINP

SEQ ID NO:26

ACE 962 Cj1019c

>AnrP326257 (NC_002163) branched-chain amino-acid ABC transport system periplasmic binding protein [Campylobacter jejuni]
 MKKLTLLSVLTMVNCLYAKDINIGVVLPLTGTVAAYGQDVNGIELANKLQPKLSNGDVIKLITIDTKG
 DXLETSNGVNRLIATDKVLGIIGEATTPTNTQIAISIAEKKIPLIAPVASGDKLLDKKKYASRVCFKDSF
 QGDKFATYVSKDLGLKNAVIIIDQSNVYSLGLARAFENSFKNNNGKIIKKLVINSGDKDFRAVVSQKSL
 NPDFVYMPHIYHPEAALIARQARQICFDKLLVAGDGVNQTFIDLGCSAVNGVIFTDSFDYNSPSTQLGKD
 FVAAYEKVKGTKELPAFSAMGADAYFVMLNAMNACVDNLSECINSKIHQTKDFQAVGGVISIDESGNAI
 RSVVIKEIQNQKQNYKTIINP

SEQ ID NO:27

ACE 984 Cj1041c

>AnrP198268 (NC_002163) putative periplasmic ATP/GTP-binding protein [Campylobacter jejuni]
 MKKYVLSLALLGSILLGASELKYQEFDGPKSPESIFVDKNYVVNVNGERKLEPLAKDNDGFISKLDKNGKV
 LEYKFLTHLNAPKGMMIEGKTLVYVDIDVLRGFDLKTKKEIFNLPPIKGAIFLNDIEKLDDNTLLVSDTGT
 GLILKVDLTKQYDELLKLDLAKFCGGPNGLYLDRKHHKLPIAGYHPDGVS GGVMAYDLNTKELSIIKNE
 KESVDGIVPYKDGLIVSSWGNNLNGYIYNLDNVKSVKLELPIMKGPAFIDIEGNILWIPKMVEGKLFKVE
 LINK

SEQ ID NO:28

ACE 1094 Cj1153

>AnrP385049 (NC_002163) putative periplasmic cytochrome C [Campylobacter jejuni]
 MKKLLVVSALACLGVSFAADGATLFFKCAVCHGANADKVYLNKPALKTLSSAERLOQYMEKEYSEGKRNA
 YGQGAIMKLNKGLTEEDFKATEAHIELTLK

SEQ ID NO:29

ACE 1155 Cj1214c

>AnrP470247 (NC_002163) hypothetical protein Cj1214c [Campylobacter jejuni]
 MFKTIIVCFIALNLSLFAVGFDLKPIKSELVKVDDIYGYIKDSDDIKLYSSGVVVOHFSNSQSIARASVI
 DDKNGLAKLEFSVFSALKQDALPFLPVLPKGDEVVLFYDRGLVIAPIKDEQTYNELVREFPQIYFTIID
 IFGAQLIRTATLSPKRSDFRQFCDDNAVGITLVVALENHAEVVDCQDFNKLYEVPIISKPTSVQVPFYSRIG
 GYKSNNFDNSQEIGNYYRYYDALINLPKVQ

P814DK00

SEQ ID NO:30

ACE 1227 Cj1287c

>AnrP530915 (NC_002163) malate oxidoreductase [Campylobacter jejuni]
 MNLKEEALKYHLGGKIDIVPSKPMATSYDLISLAYSPGVAEPCLEIAKDNELAYTYTNKANLVAIVSDGSA
 VLGLIGNIGAQASKPVMEGKACLFKKFANVNAYDIEINVHSIEEIVNFCKALAPTVGGINLEDIAAPKCFE
 IEAALQDLGIPVMHDDQHGTAIISTAGLMNAMEISGKCKFDIKVVVSGAGAAGIASAKMYRNLGVENIIL
 VDSKGVIISKDRNDLTPQKLEFAVDSKEKTLKEVLKGADVFLGLSAPKILDEMVLSMAXDPVIFALANPI
 PEVMPEDVARLRKDAIVGTGRSDYPNQINNVILGFPPIFRGALDVRAVKITENMKVAAAKALADIAKLPVS
 DAVKKAYNLSTLEFGRDYVIPKPFDERVKAAVSTAVAAAALKDGVAVKVNFDEKAYFESLK

SEQ ID NO:31

ACE 1320 Cj1380

>AnrP108003 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKKLSLILVCSASLFAASNSEISDFYSKSIIKAQFPNATSVSNRQKVGNTPFESVIVSVELNGQKQENIL
 FTKDSLITPDLDLKTGISYAQBYEMKKFQBARFNFTKNAKAVAQKETMVIALGDQNKPAIYVFSDPECP
 YCREHLAQTDDDELKNYQVNLYILTPVHGKSAFEKSALIYKEAKKAKNDKEKIAILNKYYDANIKNYPKVSD
 AELKEVFSLYEKYRSLGLSATPTIIK

SEQ ID NO:32

ACE 1431 Cj1496c

>AnrP947055 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MIKKFILLVFISSVVFGABQDCEQYFPEARAKQIELQTRFDEARQSILEYAKASFEALQKERLENLEKKEA
 EVNATLAKIEELKLENARLVEEQQQKILNSINDKTQGRVKEIYSQMDAAIADVLSQMDAEDASKIMLSLE
 SRKISGVLSKMDPKKASELTLLKNLDNNASN

SEQ ID NO:33

ACE 1449 Cj1516

>AnrP407504 (NC_002163) putative periplasmic oxidoreductase [Campylobacter jejuni]
 MNRRNFLKFNALTLASMGVAYANPMHDHMHSMHKNHSINHDLDTSFINFAPKNLKLLDPKQFPQGEILKAL
 PLLKNESKEKNIFRATLEIENHIELIKGKKTLYTNYGLVPAPKIEVPEGDKLEILVKNNLKEATTIRW
 HGVPVPPDQDGSPHDPIAGEERIYRPEIPQDSAGTYWYHPHPYTASQVFMGLAGAFVIAKQDALSH
 LKEKDOLMISDLRLDENAQIPNNNLNDWLNGREGEFVLINGQFKPKIQLATNERIRIYNATAARYLNRLIQ
 GAKFILVGTDGGGLIEKAIYKEELFLSPASRVEVLIDAPKDGDNFKLESAYYDRDKMMVKEESNTLFLANTIN
 LKKEKLELPKNLKIIFKPLEEPKEFKEIIMSEDHMQMHGMMGKSENEKLIALASMFLINGKSYDLKRIDLS
 SKLGVVEDWIVYINKSHMDHPFHIGTQFELLISSKLNGKVQKAEPRAFRDTINVRPNEELRLKMQDFKGL
 RMYHCHILEHEHDLGMMGNLEVKE

SEQ ID NO:34

ACE 1469 Cj1540

>AnrP818860 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKKIISLALALALSASAELKMATTTSTDNTGILDAKELYEKESGNTLKWVAVGTGAALKMGEDCNADV
 LFVHSPKAEEKEFMKKGFGVDRTPVMYNDFIIIADKSLASKFKGKNLKESLELIKNEKLTFIGRGDKSGTD
 NKEKSLWKNLGGVFEKQSWYQQSGQGMLASIKIAEEKKVILTDRTGYIKYEANEKGKPVLVIVNEGDDS
 LKNFYSVIATNPKECKNVNYTEASKFIKWWVTSKTLNFIADFKLLNKPLFVIDAKTRKD

SEQ ID NO:35

ACE 1584 Cj1659

>AnrP294550 (NC_002163) periplasmic protein p19 [Campylobacter jejuni]
 MIKKVLSVAAAIVISTNLPAGEVPIGDPKELNGMELAAVYLQPIEMEPRGIDLAASLADIHLHEADIHAL
 KNNPNQGFPGEFWMPYLTIAVELKNTDTGAIKRGTLMPMVADDGPHYGANIAAMEKDKGGFGVGNYELTFY
 ISNPEKQGFGRHVDEETGVGKWFEPFKVDYKFKYTGTPK

P814DK00

SEQ ID NO:36

ACE 1569 Cj1643

>AnrP407676 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKKILIIICMLFTLSPGTIERPKTFEDFLAGYERNKASMLNVEGMPAFASENLLAVLKQPNAKLNKVVKYDP
 FLNLVLYVRTDLSLIPTPMGDEEKLTTRNDWVGITWDPNKDYIGB1KYLQAQNIIDEKDQLDFNSKIGLLGTPCC
 EMMGIALNNSSFIGNRYLKHFMKVNDDVYWGDIGVDFVVRRENKIYVNNVRKNPQFLINDQVISVDGLPAND
 LRKLNEKTLFADRGSTLYFQVLRDNMDLNISTEVFKRDLSKPNLPDSKPCKPKITNPTSNLGLTVNASLUV
 TKIDPKSKVSNAGFMVGDKILRVNNIILNNFKELONILSAGNDFSILLERKSTKLPLSNFNNELGGNANS
 GGDGKFQFFIRLTK

SEQ ID NO:37

ACE 96 Cj0105

>AnrP750295 (NC_002163) ATP synthase F1 sector alpha subunit [Campylobacter
 jejuni]
 MKFKADEISSIIKERIENFDLNLEIEETGKIIISVADGVAKVYGLKNIMAGEMVFENGDKGMALNLEESS
 VGIVILKGEGGLKEGASVKRLLKPVGEALIGRVMALGEPIDAKGVINANEYRFVEEKAGIMARK
 SVHEPLHTGKIAIDALVPIGRGORELIIIGDRQTGKTTVAVDTIIISQRGQGVICITYVAIGQKQSTVAQVVK
 RLEEHGAMEYTIVVNAGASDPAALQYLADYTGVTMGEFFRDNAKHALIVYDDLSKHAVAYREMSLILRRP
 PGREAYPGDVFYLHSRLLERASKLNDLGAGSLTALPILETQAGDVSAYIPTNVISITDGQIFLETIDLNFN
 SGIRPAINTVGLSVSRVGGAAQIKATKQVSGTLRLLAQYRELQAFQFASDLD2ASRKQLERGQRMVELL
 KQPPYSPLSVEKQVVLIFAGTKGFLDDIAVSRIKEFEDGIFTPEAKHPDIFEQIRSKKKALDSLEEKLA
 KAINEFKANHL

SEQ ID NO:38

ACE 165 Cj0175

>AnrP550554 (NC_002163) putative iron-uptake ABC transport system periplasmic
 iron
 MKKIFFMFLTAVSFLGASELNIYSARHYNADPEIILKKFEEKTGIKVNUHTQAKASELIKRLSLEGSNSPAD
 IFITADISNLTEAKNLQLLSPVSSKYLEEFTPAVLRDXDKGEWFAITKARILAYNIKNTNIDISIGMGNYED
 LAKAEFPKGHIIVMR9ATAFYSKTLIAGSLIANDGNKEAKAWAVGVLENLATNPKGGDRDQARQVTAKEAICA
 VMNTYYIGLLKNSKNPKDVEVGNSLGIIIFPNQDNRGTIHINTSGIAMTKSSKNQDAAKKFMEFMLSPEIQK
 ILTDSNYEFFIRNDVELSQTVKDFGTFKEDQIPVSKIAENIKEAVKIFYDEVGFR

SEQ ID NO:39

ACE 257 Cj0283c

>AnrP602342 (NC_002163) chemotaxis protein [Campylobacter jejuni]
 MSNEKLEQIILQKQQTQMAGPDVDQREDDIIQLVGFVVGDEEYAIPILNQEIILKPIBYTRVPSVPDYVILG
 VFNMRRGNVMPMLIDLAQRFHLGSSKMTPQTRYIVLGETNGTGVGGNAGFVIDRILTEAIKIHRNRIDPPP
 TLVKDKGMIFYGICKRDENILTILKVEALLKREF

SEQ ID NO:40

ACE 277 Cj0303c

>AnrP311344 (NC_002163) putative molybdate-binding lipoprotein [Campylobacter
 jejuni]
 MKKFVVVPGILLFVSCLNAQNLSIFVASSASKAMSEVKDEFLKTHPZDKIELVFGASGKYELLKQGREF
 DLFFSADTKYAKAIYDKNALIKPKVYVLGVIALVSLIENLLQGGVENLKEKANKITHLSIANPKVAPYG
 VAAKEVLENLGLINELLKDKIVLGENISVPVLHVDSKNSDIAIVAYSLSVSSINHPKGKAVIIDAKYFSPL
 QSYVITKAYADICKLAFEFNEFIGSSKAKEIFKKYGFSTE

SEQ ID NO:41

ACE 308 Cj0334

>AnrP505685 (NC_002163) alkyl hydroperoxide reductase [Campylobacter jejuni]
 MIVTKKALDFTAPAVLGNNETIVQDFNLYKNIGPKGAVVFFYPKDFTFVCPCSEIIIAFDKRYQEFPKNRGIEV
 IGISGDNEFSHFAWKNTPVNQGGIGGVKFLPLADLTQKIAARNFDVLYAEAVLRSFLIDADGTVRHAVV
 NDPLPLGRNIDEMLRMVDTMLFTNEHGEVCPAGWNKGDECMLKANPKGVAEYLKGNEAKL

P814DK00

SEQ ID NO:42

ACE 388 Cj0415

>AnrP72219 (NC_002163) putative oxidoreductase subunit [Campylobacter jejuni]
 MAEVLKVKDVVTVGAGWIGGIVAAELTKAGILNVLSLERGHMQSTENFNYIHDEWRYGINYGLMDCSKDT
 VTFRHDPGDLALPYRKMGSFLLGNVGGAGVHWNGWTFRFMPYDFEIQTLSKQRYGNKLGNNDYTTLQDWGV
 TYKDMEPYYDRFEKTCGVSGEPNPLAEKGMAFRSSPPYDQEPLENTKMLKRPESAACKSSNLHTYRLPASN
 KGGYTNPDQDLPACQYCAYCERFGCEYAKASPLNTVTPKAMSTGKYTIRTYSNVTQILKKDGKVTVGK
 FVDTRTMKEYIQPADIVVLTSMFNNAKLIMVSNIQEYDPKTGKTLGRNYCVQNMGTIAFFDEQFNT
 FMGSGALGTTSDDFNGDNFDHSKEKFLEGAMIYSVQLGTRPIQSAPLPGAPTWGAFFKKALNYNFTRAI
 TVGGQGASILPHKNNYLSDLPTYKDAFGMPLLRLTYNFTDQDRALHKFITDKTAEVAKRMQGVKS1KKGAY
 LKDYSVVPYQSTHNTGGTTMGADRETSVVNTYLQHWDADNLFVVGAGNPFQHNSGYNPTDTV GALAVRCAE
 GILKYHKSGKSLA

SEQ ID NO:43

ACE 393 Cj0420

>AnrP490750 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKKVLLSSLVAWSLLSTGLFAKEYTLDAHDKAHTDVGFKIHLQISNVKGNFKDYSAVIDFDPASAEFKKL DV
 TIKIASVNTEQTRDNHLQODDFKAKKYDMDTFTMKKYEKIDNEKGKMTGTLTIAGVSKD1VLDABIGG
 VAKGKDGEKIGFSLNGKIKRSDFKFATSTSTTILSDDINLNIEVEANEK

SEQ ID NO:44

ACE 711 Cj0759

>AnrP596832 (NC_002163) heat shock protein dnaK [Campylobacter jejuni]
 MSKVIGIDLGTTINSCVAVYERGESKVIPNKEGKNITPSVVAFTDKGEVILVGDSAKRQAVTNPEKTIYSIK
 RIMGLMINEDAACEAKNRLPYHTTERNGACAIETIAGKITYTPOBISAKVLMKLKEDAEFLGESVTDavit
 VPAVFNDAAQRKATKEAGTIAGLNLVRITINEPTSAAALAYGLDKKDSEKIVYYDLGGGTFDVTVLETGDNVV
 EVLATGGNAFLGGDDFDNKLIDFLANEFKDETGIDLKNDVMALORIKAEEAENAKKELSSANETEINLPI
 TADASGPKHILVKKLTRAKFEGMIDSLSVAETITKINEVVSIDAGLKKDEIKEIVMVGGSTRVPLVQEEVKRA
 FNKDLNKSVNFDEVVAIGAAIQGAVIKGDVKVLLDVTPLSLGIELTGGVMTKIIIEKGTIPTKKEQVF
 STAEDNQSAVTINVLQGEREFSRDNKSLGNFNLEGIPPAFRGMPQIEKVTFDIDANGILTVSAKD KATGKA
 QEIKitGSSGLSBEETINNMVKDAELHKEEDDKRKEAVDARNAADSLAHQVEKSLSELGEKVAADKENTIQ
 KALDDLIRETILKNQNASKBEIESKMKALSEVSHKLAENMYKDEPTANDKKKKDDDVDAEVE

SEQ ID NO:45

ACE 723 Cj0771c

>AnrP524051 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MNLFKIIILACILNLSSLFAQNTITIGATTPNPFGSLLLEMKDDFKNKGYELKIVEFSDYILPNRALEKKEL
 DANLYQHKPFLBHYNLKKGSNLIAATTVPVLIAPVGVYSKKIKNLENLKEGARVAIPNDPTNESRALELLEK
 AKLIELNKNTLKTPLDINKNPKKLKFIELKAAOLPRAIDDVDIAIINSNPALGAGLNPSKDTIFREDKNS
 PYVNYVVVRSEGKNSEKTKVIDHILRSDFKAIINEHYKDILIPAF

SEQ ID NO:46

ACE 724 Cj0772c

>AnrP579672 (NC_002163) putative periplasmic protein [Campylobacter jejuni]
 MKIKSLPIASILTSLNANALETITVAATPVPHAEILEQVKPDLEKQGYKLEIKBFTDYVLPNLAVDNGE
 ADANFFQETPTYLEEFNKNKGTKLIKVAAIHIEPMAVYSKKYKSLDDIKEGVKIAIPNDPTNESRALDIIA
 KKGLVKFKDKALKTPLDIIDNPKKIKFVELKPAQLPRA LDVDFAVINSNYALSANLNPASKDSVFI EKE
 SPYANILVVVRVGHENDPKIKALIQLQSDKIKQFIIKEYNGSVLPFAF

SEQ ID NO:47

ACE 819 Cj0872

>AnrP694298 (NC_002163) putative protein disulphide isomerase [Campylobacter jejuni]
 MRNPFCKFVLALVFYSSPALANNSFITLNPSLPSSENSVIEAFSYKCICH CYNHKKFGTLEKLREA FPNLH
 FKLYFVSLMNMGESFSKEMNELFTFAQYKDEQNGKDA SYSDSLSHKLADVYFVSYFLNKQRFNSNLDBFYDI
 GLKAMNVNKNEVLNFLNTPKAKSILSEFQRANDIAKTYGTPAFVUNGKYQINPSAINSMQDLEDLVKKLS
 NMK

P814DK00

SEQ ID NO:48

ACE 1060 Cj1118c

>AnrP515430 (NC_002163) chemotaxis regulatory protein [Campylobacter jejuni]
 MKLLVVDDDSSTMRRIIKNTLTRLGHDDVLEAEHGVEAWLLTKNEDVKVLITDWNMPEMNGLELVKKVRA
 EKKYEDMPIIMVTTEGGKAEVITALKAGVNNYIVKPFTPQVLKEKLEDVLGTGSCEGAAE

SEQ ID NO:49

ACE 1169 Cj1228c

>AnrP679791 (NC_002163) serine protease (protease D0) [Campylobacter jejuni]
 MKKIFLSLSLASALFAASINFNESTATANRVNPAAAGNAVLSYHDSIKDAKSVVNISTSKTITRANRSP
 LIDDFNDPYFKQFFDFDFDSQRKGKNDKEVSSSLGSGVIISKDGYIWTNNHHVVDADTTIVNLPGSDIEYK
 AKLIGKDPTKTDLAVIKIEANNLSAITPTNSDDLMEGDVVFALGNPPFGVGFSVTSGIISALNKDNIGLNQY
 ENFIQTDASINPGNSGGALVDSRGYLVGJNVALYRGGGNNGIGFAIPSNMVXDIANKLIEKGKIDRGEFL
 GVTILALQGDTKKAYKNQEGALITDVQKGSSADEAGLKRGDLVTKVNDKVIKSPIDLKNYTGTLEIGQKI
 SLSYERDGENKQASFILKGKEKENDKGVQSDLIDGLSLRNLDPRLKORLQIPKDVNGVLVD SVKESKGKN
 SGFQEGDIIIGVGQSEIKNLKDLHQALKQVNKEFTKWWVYRNGPATLLVLK

SEQ ID NO:50

ACE 1510 Cj1584c

>AnrP355324 (NC_002163) putative peptide ABC-transport system periplasmic peptide-
 MLRFVLLFLFLNLEAKIPKDTLIAVENETIARINPAYSEDHDavinLVFSQLTRFDENMSLKPDLAKS
 WDISKDGIVYDIFLRDDVLWHDGVKFADDVKSIEAFKPNPKNSIYIVNFEDIKSVEILNPShVKITLF
 KPYPAFLDALSIGMLPKHLLNEENIINTSSFNQNPIGTGPYKFWKKGEYVEFKANEHFYLDKVKTFRLI
 IKHIFDPSTIASAELKNGKIDAALIDVSLLNIFKNDENFGILREKSADYRALMFNLNEFLKDLKVRQALN
 YAVDKESIVKNLLHDYAFVANHPLERSWANSKFKIYKYDPKKAEDLLVSAGFKKQKDGNEFKDGKILEF
 EIWAWSNDPLRVSLAGILQSEFRKIGVVSKVVAKPAGSFDDYSKVDLSFLIGWGSPLDPDFHTFRVPESQD
 SALNDEGWNFGHYHDKKVDIALQKARNTSNLEERKYYKDFIDALYENPPFIELAYLDFALVINKDLKGI
 KTRTLGHHGTVGFTWNVXEWSK

SEQ ID NO:51

ACE 1543 Cj1617

>AnrP111949 (NC_002163) putative haemin uptake system periplasmic haemin-binding protein [Campylobacter jejuni]
 MKKILIIMSLFLIALNAKERLVVLDPASIELFMLKAEDQIVGIATLQHSNIYPKDQTSKLTSVGTFSNP
 SLEKIVALKPSLVLISLSSYSLNLEEGLKNFGIKSINLKAERLEDITKNTTLGQITKKEKEAELLKQEPNO
 KFKKLSDKPLNKSAYLYSSNPLMAFNDNSLIADILRLIGIKNLSPSQISRPVISAEYILKQNPDLIL
 GINAKNNLDTNALLKNTKAVKTGSIVFNKDTPLLRLSPKIIDRIQEFTKLENNNF

Fragments of AnrP630851 (Cj0092)

SEQ ID NO:52: TQQDINTQNEMSDASTKDITPKSIEDFFEEFAD
 SEQ ID NO:53: GITKDGTFYTGKSTYAVNDTDFQF
 SEQ ID NO:54: RIATSKIQNYEADNSTNAKEFDELPKGDKVDQILNK
 SEQ ID NO:55: QLDKALKDLGIDTNSLSEDRKKTLLKQEFILNKTMTN
 SEQ ID NO:56: TIVTQRRGEYDVGVVAVISNKTRQLAKD
 SEQ ID NO:57: AISEYLPKDTKGFLNEYGIRLVYDEN
 SEQ ID NO:58: DPSNAKKTNIILEDRAKE
 SEQ ID NO:59: LSLKDERTTGDTYEEE
 SEQ ID NO:60: VNDSSTQBQTQNITN
 SEQ ID NO:61: TLKKWSYTSENG
 SEQ ID NO:62: Y5YENLANTNEALNSKSNTAKKSSSIQRS

P814DK00

Fragments of AnrP57234 (Cj0143c)

SEQ ID NO:63: IFYTFTQAKNLBQEQNNTSSNLVSVS
 SEQ ID NO:64: LPPNSNEHNFEFKPSTMKKLEKSDIVF
 SEQ ID NO:65: LEPEKVFTDKFKQNFPKLQVINMQ
 SEQ ID NO:66: IOTHDTHEHSHEHHHHHHGHGHPHTWL
 SEQ ID NO:67: DTLIQKYPQNEONLYKENLDK
 SEQ ID NO:68: SKLEKLQNRE
 SEQ ID NO:69: YPAKRYNL
 SEQ ID NO:70: GKEPKSKDLQK
 SEQ ID NO:71: LMKDKNLK
 SEQ ID NO:72: QNGFPENAAKTFLAKECDAKIYK
 SEQ ID NO:73: DHLSYDWENELLKTADAF

Fragments of AnrP490750 (Cj0420)

SEQ ID NO:74: FAKEYILDAHTDVGFKIKELQI
 SEQ ID NO:75: VKGNFKDYSAVIDFDPASAEPKKLDVTI
 SEQ ID NO:76: SVNTENQTRDNHLQQDDPF
 SEQ ID NO:77: DFFKAKKYPDMLFTM
 SEQ ID NO:78: TFTMKKYEKIDNEKGKMT
 SEQ ID NO:79: GVAKGKDGEKEKIGF
 SEQ ID NO:80: LNGKIKRSDFKFATPS
 SEQ ID NO:81: EVEANEK

Fragments of AnrP684299 (Cj0715)

SEQ ID NO:82: LSATEYQLSTHV
 SEQ ID NO:83: ITSGQPARKVKVBLYK
 SEQ ID NO:84: LEANQQWKKVSEEFTEENGRIG
 SEQ ID NO:85: LLPYEAENRAFG
 SEQ ID NO:86: KFFTQDXYTSHKINTF
 SEQ ID NO:87: SFELSKDQKHVHYHPI
 SEQ ID NO:88: FGYSTYRGS

Fragments of AnrP579672 (Cj0772c)

SEQ ID NO:89: ILEQVKPDLEKQGYKLEIKBFPTDY
 SEQ ID NO:90: GEADANFFQHTPYLEEFNKNKGT
 SEQ ID NO:91: AVYSKKYKSLLDIKE
 SEQ ID NO:92: IPNDPTNESNO
 SEQ ID NO:93: KGLVKFKDKALKTPLDIIDNPKKIRFVELKPAQLPRLN
 SEQ ID NO:94: ANLNPAKDSVFIEDKESPYAN
 SEQ ID NO:95: GHENDPKIKALIQALQSDKIKQFIEKYN

Fragments of AnrP257863 (Cj1018c)

SEQ ID NO:96: NGDKVSLAITDTKGDKLESSSGANRLVSQLK
 SEQ ID NO:97: VAEDNKIPLIAPAATGDRILLDKKIYSSRVC
 SEQ ID NO:98: YVFSKLNKBAVIVVDQSTDYSLGLAKAFEQYKSNGGQ
 SEQ ID NO:99: NSGDKDPRAIVAQVKSLNPEFIFLFLYYSEASLFARQSKLA
 SEQ ID NO:100: GYIFTDSFDANNPTTKLSKEFISVYEKAGTKEVPNFSAMG
 SEQ ID NO:101: VNEKIHQTKNYQGV
 SEQ ID NO:102: QTGNATRSVVVKEIKNQKONYKOTIN

Fragments of AnrP108083 (Cj1380)

SEQ ID NO:103: ELNGQKQENILFTK
 SEQ ID NO:104: SYAQEYEMKKFQEARENPTXNAKAVAQKETM
 SEQ ID NO:105: VIALGDKNPKAI
 SEQ ID NO:106: HLAQIDDELKNYQV
 SEQ ID NO:107: YKEAKKAKNDKEKIAI
 SEQ ID NO:108: LNKYYDANIKNYPKVSDAELKBVFSLYBKYRSL

P814DK00

Fragments of AnRP407676 (Cj1643)

SEQ ID NO:109: GIERPKFEDFLAGYERNKASMLN
SEQ ID NO:110: LKQPNAKLNKVVKYDPFL
SEQ ID NO:111: PTPMGDEEKLTRNDWVGIWDPNKPYI
SEQ ID NO:112: AQNIDEKDQDFNSK
SEQ ID NO:113: GNRYLKHFMICINDVY
SEQ ID NO:114: VVRENKIYVNNVRKNPQFL
SEQ ID NO:115: PANDLRKLNEK
SEQ ID NO:116: DRG9TLYFQVLRDNMDLN
SEQ ID NO:117: AKDLSKFNLPDSDKPKPKI
SEQ ID NO:118: TKIDPKSKVSNAG
SEQ ID NO:119: LIERKSTKLPLSNFN

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